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AAY03165 standard; protein; 13 ₽

ALIGNMENTS

AAY03165;

11-JUN-1999 (first entry)

Linker used in Chimeric sIL-6R/IL-6 protein.

Soluble interleukin-6 receptor; interleukin-6; sIL-6; IL-6; sIL-6/IL-6; chimeric protein; fusion protein; cell growth inhibitor; melanoma cell; highly malignant cancer cell; in vivo engraftment; mammalian cancer; human haematopoietic cell; bone marrow transplantation; mammalian cancer; hepatotoxic agent protection; haematopoiesis; liver disorder; hepatotoxic agent protection; neurological disorder.

Synthetic

WO9902552-A2

21-JAN-1999

09-JUL-1998; 98WO-IL000321.

10-JUL-1997; 30-DEC-1997; 97IL-00121284. 97IL-00122818.

(YEDA) YEDA RES & DEV CO LTD.

WPI; 1999-120776/10.

Revel M,

Chebath J,

Lapidot T,

Kollet 0

New glycosylated soluble IL-6 receptor/IL-6 conjugates - used for treating cancers, bone marrow transplantation, increasing haematog or treating liver or neurological disorders. used for e.g. haematopoiesis

Claim 5; Page 54; 77pp; English.

RESULT 1
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AC AAYO
AC AAYO
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KW Chim
KW high
KW high
KW hew
PH New
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XX WPI
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CC Thi
CC SIL
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CC SIL This sequence represents a linker that can be used in the chimeric glycosylated soluble interleukin-6 receptor (sIL-6R)-interleukin-6 (IL-6) protein (sIL-6R)-1.5 of the invention. The sIL-6R/IL-6 protein comprises a fusion protein product between all of the naturally occurring form of sIL-6R and all of the naturally occurring form of sIL-6R and all of the naturally occurring form of IL-6, the sIL-6/IL-6 and analogues being glycosylated in a similar fashin to the glycosylation of naturally occurring sIL-6R and IL-6. The sIL-6R/IL-6 and analogues are capable of inhibiting the growth of highly malignant cancer

Streptomy

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RESULT 2
AAU11643
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The invention describes the use of interleukin-18 (IL-18) inhibitor for manufacture of medicament for treatment and/or prevention of diseases or diseased conditions of the arteries, heart failure recurrent events, or as diagnostic marker for bad cilinical prognosis in heart failure or recurrent events after first event of heart failure. The IL-18 inhibitor prevention of atheroscierosis/arteriosclerosis, the manufacture of a medicament for treatment and/or medicament for treatment and/or prevention of theorem, as therefore the plaque (AP), Ap ulcer, AP destabilisation (responsible for stroke), atheroma, is chaemic syndromes e.g. myocardial infarction, AI ischaemia, re-vascularisation and progression of atherosclerosis, where the heart failure is ischaemic or non-ischaemic and as a diagnostic
                                                                                                                                                                                                                                                                    Use of interleukin-18 inhibitor for manufacture of medicament for treatment and/or prevention of atherosclerosis, thrombosis of atherosclerotic plaque, atherosclerotic plaque ulcer and heart fair
                                                                                                                                                                                                                                    Disclosure; Page 16;
                                                                                                                                                                                                                                                                                                                                                                              Chvatchko
                                                                                                                                                                                                                                                                                                                                                                                                             (ISTF )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             interleukin 18; IL-18; cytokine; interleukin-18 inhibitor; atherosclerosis; cardiant; vasotropic; antiulcer; myocardial infarction; atherosclerotic plaque; thrombosis of atherosclerotic plaque; stroke; ischaemic syndrome; heart failure; arteriosclerosis; vascularisation; atheroma; immunoglobulin; linker peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-MAY-2000;
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The present invention relates to the use of human secreted apoptosis-
CC related protein 1 (SARP-1), SARP-1 nucleic acids and/or a substance which
CC stimulates the release or potentiates the activity of endogenous SARP-1
CC for the treatment of scleroderma. The SARP-1 protein binds to and
CC initiates signalling of the human SARP-1 receptor. The SARP-1 protein can
CC be used in protein therapy, and the polymucleotide sequences encoding
CC sequences, and pharmaceutical compositions comprising SARP-1 are useful
CC sequences, and pharmaceutical compositions comprising SARP-1 are useful
CC for the treatment of scleroderma, especially systemic sclerosis. They may
CC interstitial pulmonary fibrosis, Dupuytren's contracture, keloid and
CC contractive fibrosis), chronic heart failure (particularly after myocardial
CC infarction), disorders involving inflammation of the lung (e.g. rheumatoid
CC arthritis). The present sequence represents a linker peptide that can be
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                                                                                                                                                                                                                                                                                                                                                                                  sclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                    Use of human nucleic acid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-DEC-2000;
17-AUG-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Secreted apoptosis-related protein 1; SARP-1; scleroderma; systemic sclerosis; fibrotic disease; liver cirribosis; keloid; interstitial pulmonary fibrosis; Dupytren's contracture; scarring; wound healing; postoperative adhesion; reactive fibrosis; chronic heart failure; myocardial infarction; inflammatory disorder lung inflammation; idiopathic pulmonary fibrosis; systemic disease; rheumatoid arthritis; anti-sclerotic; immunoglobulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plater-Zyberk C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-NOV-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ISTF )
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Secreted apoptosis-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABG70576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               marker for bad clinical prognosis in heart failure or recurrent evalue first event of heart failure. This sequence is an example of peptide linker used to create fusion proteins of Interleukin-18 (1) with all or part of an immunoglobulin, discussed in the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EFGAGLVLGGQFM 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLIED RES SYSTEMS HOLDING
                                                                                                                                                                                                                                                                                                                                                                                  Secreted Apoptosis-Related Protein (SARP)-1 and SARP-1 s for the treatment of sclerosis, especially systemic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000EP-00126771.
2001EP-00118888.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2001WO-EP013992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   inflammatory disorder;
sis; systemic disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linker peptide
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(IL-18)
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ARESULT 4
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ABR44230
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AAY25368
ID AAY2
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Best Local
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                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to the use of a substance (I) signaling through gpl30, or use of a vector (II) for inducing and/or enhancing the endogenous production of interleukin-6 (IL-6) in a cell. (I), (II) or cell expressing (I), is useful in the manufacture of a medicament for treatment and/or prevention of diabetic neuropathy. (I) is useful for treating or preventing diabetic neuropathy such as polyneuropathy or mononneuropathy. The present sequence represents a linker peptide used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Linker peptide used in constructing
                         AAY25368
                                                                                                                                                                                                                                                                                                                                                 Sequence 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 17; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Use of a substance signaling through gp130, or use of a vector for inducing and/or enhancing endogenous production of interleukin-6 in for preparing a medicament for treating and preventing diabetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-403150/38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dreano M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-AUG-2003
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                                                                                                                                                                                                                                                                                                                                                                                                  constructing an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              neuropathy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-OCT-2001; 2001EP-00123400.
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13; Conserv
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                                                                                                                                                                           EFGAGLVLGGQFM 13
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                       standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EFGAGLVLGGQFM 13
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                                                                                                                                                                                                                                                                                                                                                 ₽,
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                                                                                                                                                                                                                                                                                                                                                                                                  IL-6R/IL-6 chimera
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                    peptide;
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                                                                                                                                                                                                                                                 Score 67; DB
Pred. No. 0.0
0; Mismatches
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Pred. No. 0.00045;
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                                                                                                                                                                                                                                                                      DB 6; 1
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RESULT 6
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XC Anti
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KW hair
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Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention describes a novel method for prolonging the in vivo effect of type I interferon (IFN) by administering IFN as a complex (A) with a subunit (I) of the human interferon alpha/beta receptor (IFNAR). The product of the invention has antiviral, anticancer, immunomodulatory, anti-arthritic and antidiabetic activity. (A) have the antiviral, anticancer and immunomodulating activities of IFN, e.g. for treating hepatitis and other viral infections, hairy cell leukemia, Kaposi's sarcoma, multiple myeloma and other cancers, multiple sclerosis, rheumatoid arthritis, myasthenia gravis, diabetes, acquired immune deficiency syndrome and lupus. When complexed in (A), the storage life of IFN is increased (i.e. it is stabilized against oligomerization, without the need for storage at acidic pH) and its biological effect is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IFNAR2; IFN-beta; type I interferon; IFNAR/IFN complex; IFN; antiviral; human interferon alpha/beta receptor; anticancer; immunomodulatory; anti-arthritic; antidiabetic; treatment; hepatitis; viral infection; hairy cell leukemia; Kaposi's sarcoma; multiple myeloma; cancer; lupus; diabetes; multiple sclerosis; rheumatoid arthritis; myasthenia gravis; acquired immune deficiency syndrome.
             IFNAR2; IFN-beta; type I interferon; IFNAR/IFN complex; IFN; antiviral; human interferon alpha/beta receptor; anticancer; immunomodulatory; anti-arthritic; antidiabetic; treatment; hepatitis; viral infection;
                                                                                                                 06-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                               Sequence 21 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Prolonging in vivo activity of type I interferon by complexing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-405115/34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IFNAR2/IFN-beta complex peptide fragment 11.
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                                                                                                                                                AAY25369;
                                                                                                                                                                               AAY25369 standard; peptide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-DEC-1997;
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                                                                                IFNAR2/IFN-beta complex peptide fragment 12.
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                                                                                                                                                                                                                                                                EFGAGLVLGGOFM 18
 leukemia; Kaposi's sarcoma; multiple myeloma; cancer; lupus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cunningham M,
                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Page 80; 86pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                               Score 67; DB 2;
Pred. No. 0.00074;
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                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                 Gaps
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RESULT 7
ABO70163
ID ABO7
XX ABO7
XX ABO7
XX Pseu
XX 18-F
PR 18-F
PR 27-;
XX 18-F
PR 27-;
XX (GET
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                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention describes a novel method for prolonging the in vivo effect of type I interferon (IFN) by administering IFN as a complex (A) with a subunit (I) of the human interferon alpha/beta receptor (IFNAR). The product of the invention has antiviral, anticancer, immunomodulatory, anticancer and immunomodulating activities of IFN, e.g. for treating hepatitis and other viral infections, hairy cell leukemia, Kaposi's sarcoma, multiple myeloma and other cancers, multiple sclerosis, rheumatoid arthritis, myasthenia gravis, diabetes, acquired immune deficiency syndrome and lupus. When complexed in (A), the storage life of IFN is increased (i.e. it is stabilized against oligomerization, without the need for storage at acidic pH) and its biological effect is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diabetes; multiple sclerosis; rheumatoid arthritis; myasthenia gravis; acquired immune deficiency syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 80; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-405115/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tepper M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUL-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                     Pseudomonas aeruginosa
                                                                                                                                                                                 Bacterial infection;
                                                                                                                                                                                                          Pseudomonas aeruginosa polypeptide #2338.
                                                                                                                                                                                                                                       29-JUL-2004
                                                                                                                                                                                                                                                                 ABO70163;
                                                                                                                                                                                                                                                                                           ABO70163 standard; protein; 360 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Prolonging in vivo activity of type I interferon by complexing
                           18-FEB-1998;
27-JUL-1998;
                                                                     18-FEB-1999;
                                                                                                                            US6551795-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV. (MCIN/) MCINNIS P G.
  (GENO-) GENOME
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                                                                                                                                                                                                                                                                                                                                                                                           1 EFGAGLVLGGOFM 13
                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
13; Conserv
                                                                                                                                                                                                                                                                                                                                                                 EFGAGLVLGGQFM 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cunningham M,
                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; ilarity 100.0%; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ă,
                                                                                                                                                                                                                                       (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97US-0068295P
  THERAPEUTICS CORP
                           98US-0074788P.
98US-0094190P.
                                                                      99US-00252991.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98WO-US026926
                                                                                                                                                                                Pseudomonas aeruginosa infection; antibacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sherris D,
                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                      Score 67; DE
Pred. No. 0.0
); Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                   . 0.0012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tayar N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 34;
                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mckenna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ß
                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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RRESULT 8
AAY37561
ID AAY3
XX AAY3
XX AAY3
AC AAY3
XX Prot
XX Prot
XX Vacc
XW Vacc
XW Vacc
XW Dart
XX Chla
XX 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to Pseudomonas aeruginosa polypeptides and the polymucleotides encoding them. The sequences are useful in diagnosts and continuous as molecular targets for diagnostics, corophylaxis and treatment of pathological conditions resulting from a coronary for the ability to bind a P. aeruginosa nucleic acid, as components of effective antibacterial targets, as targets for antibacterial drugs, coincluding anti-P. aeruginosa drugs, as templates for recombinant components for diagnosis and/or treatment of P. aeruginosa-derived peptides or polypeptides, as target components for diagnosis and/or treatment of P. aeruginosa-caused components for diagnosis and/or treatment of P. aeruginosa-sequences AB667826-CC AB084396 represent P. aeruginosa polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                   28-NOV-1997;
17-DEC-1997;
04-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             paratrachoma; inclusion conjunctivitis; genital disease; perihepatitis;
nongonococcal uretritis; epidymitis; cervicitis; salpingitis;
bartholinitis; pneumopathy; venereal lymphogranulomatosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vaccine; eye disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein involved in intermediate metabolism of fatty acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY37561 standard; protein; 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rubenfield MJ,
                                                                                              Griffais R;
                                                                                                                                                                                                                                                                                                                                               27-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                             10-JUN-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chlamydia trachomatis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seqdata.uspto.gov/sequence.html
                                                                                                                                                            (GEST ) GENSET
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8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nolling
                                                                                                                                                                                                                                                       97FR-00015041.
97FR-00016034.
                                                                                                                                                                                                                                                                                                                                                  98WO-IB001939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  conventional trachoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18909; 455pp; English.
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    Mismatches

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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ú
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bush
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nonendemic trachoma;
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WPI; 1999-371125/31.

sequence

of Chlamydia trachomatis

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RESULT 9
ADM98607
ID ADM9
XX ADM9
XX ADM9
XX Gera
XX Gera
XX Gera
XX Gera
XX Gera
XX Poll
XX Poll
XX Poll
XX N US2C
XX US2C
XX US2C
XX US2C
XX HAN
XX WAL
PL MAC
PR WPI
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PT Gera
PX Cla
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CC enc
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                                                        The invention relates to a unicellular organism for producing a diterpene or diterpene precursor comprising an exogenous nucleic acid sequence encoding a geranylgeranyl pyrophosphate synthase under the control of a promoter operable in the organism, and an exogenous nucleic acid sequence encoding a diterpene synthase under the control of a promoter operable in the organism. The invention also relates to methods of producing a the organism.
                                                                                                                                                                                                                                              New unicellular organisms comprising exogenous nucleic acids encoding geranylgeranyl pyrophosphate and a diterpene synthase, useful for producing diterpenes and diterpene precursors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-JAN-2002; 2002US-00041018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chlamydia trachomatis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Geranylgeranyl pyrophosphate synthase; diterpene; diterpene precursor; diterpene synthase; defence toxin; volatile defensive signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Geranylgeranyl pyrophosphate synthase polypeptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 199 AA;
diterpene or diterpene precursor and a method of isolating a diterpene synthase comprising growing several cells in the presence of a polyaromatic resin to make a cell/resin mixture, where at least one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JAN-2001; 2001US-0259880P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US2004072323-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                        MATS/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                    2004-373921/35.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        MATSUDA S P
                                                                                                                                                                                                                                                                                                                                                                                                                      HART E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FGVGGILGGQY 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            attractant;
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                                                                                                                                                                                                           IJ
                                                                                                                                                                                                                                                                                                                                                                           Hart EA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein;
                                                                                                                                                                                                         27; 38pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            photoprotectant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            enzyme.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 199;
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The invention relates to multiprotein complexes from eukaryotes. Proteins of the invention and DNA sequences encoding them are given in records ABR52568-ABR53903 and ACC60610-ACC61944 respectively. The complexes are obtainable by using a protein as a bait and isolating the set of proteins which is attached thereto from cells. Such protein complexes may comprise up to 30 distinct proteins. Protein complexes of the invention are useful for diagnosing a disease or disorder, or as a target for an active agent of a pharmaceutical, preferably a drug target in the treatment or prevention of a disease or disorder. Note: The sequence data for this

New isolated protein complexes useful for diagnosing a disease or disorder, or as a target for an active agent of a pharmaceutical, preferably a drug target in the treatment or prevention of diseas

SEQ ID

NO 1141; 17pp + Sequence Listing;

English

of disease

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N-PSDB;

2003-250078/25.

ACC61180

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ARESULT 10
ARES3138
ID ARES3
XX ARES3
XX ARES3
XX Prote
XX Multi
XX Multi
XX Sacch
XX Sacch
XX PF 20-DE
XX PF 20-DE
XX PF 20-DE
XX CELL
XX WPI;
DR WPI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gavin A, (
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                                                       conditions. The protein complexes are useful as targets for an active agent of a pharmaceutical. These protein complexes are particularly useful as drugs targets for the treatment or preventing of a disease or disorder. The complexes and methods above are useful in diagnosing or screening for the presence of a disease or disorder or a predisposition for developing a disease or disorder in a subject. These are also useful in screening for a drug for treatment or prevention of a disease or disorder. The molecule that modulates the amount, activity or protein components of the complex is useful for the manufacture of a medicament for the treatment or prevention of a disease or disorder. This sequence corresponds to a protein of the invention. (Note: the sequence data for this patent did not form part of the printed specification but was obtained from the EPO in electronic format).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    second protein, or its derivative, fragment, homologue or variant. The proteins are selected from given protein complexes, which are not defined in the specification. The variants are encoded by nucleic acids that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New proteins and protein complexes from eukaryotes, useful as targets drug screening, or in diagnosing or screening for the presence of a disease or disorder, or a predisposition for developing a disease or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 1351; 13pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hybridize to the nucleic acids encoding the proteins under low stringency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to novel protein complexes comprising a first and a
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DB; ADK63101.
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                                                                                                                                                                                                                                                                                                                                                    The invention relates to Pseudomonas aeruginosa polypeptides and the polynuclectides encoding them. The sequences are useful in diagnosis and therapy of pathological conditions, as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from a bacterial infection, for evaluating a compound, such as a polypeptide, for the ability to bind a P. aeruginosa nucleic acid, as components of effective antibacterial targets, as targets for antibacterial drugs, including anti-P. aeruginosa drugs, as templates for recombinant production of P. aeruginosa drugs, as templates for recombinant components for diagnosis and/or treatment of P. aeruginosa-caused infection, and in detection of P. aeruginosa sequences or other sequences of Pseudomonas species using biochip technology. Sequences ABO67826
                                                                                                                                                                                                                                                                    ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection.
                                                                                                                                                                                Sequence
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27-JUL-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pseudomonas aeruginosa polypeptide #10971.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AB078796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABO78796 standard; protein; 640 AA
                                                                                                                                                                                                                                        seqdata.uspto.gov/sequence.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GENO-) GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      194 EFGASVIAGGQ 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  l Similarity
7; Conserv
         2 FGAGLVLGGQ 11
                                                             Similarity
8; Conser
                                                                                                                                                                                   640
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                 Conservative
                                                                                                                                                                                   A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         THERAPEUTICS CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98US-0074788P
98US-0094190P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9908-00252991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nolling J,
                                                                                            61.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Deloughery C,
                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 41;
Pred. No.
                                                                                            Score 41;
Pred. No.
                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                               4.1e+02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2
                                                                                                                        Length 640;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 623;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0,
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                                                                 Gaps
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RESULT 13
AAB66456
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                                                                                                                                                                 treating an individual suffering from a mycobacterial infection, consuperted of being infected with a Mycobacterium, or having been exposed to an infectious Mycobacterium. It is also useful for identifying and isolating mutants of actinomycetales and for identifying compounds that have antibiotic activity. The method is used to identify mutants of microorganisms, preferably an actinomycetales, such as M. tuberculosis, M. bovis, M. leprae, M. avium, M. intracellulaire and M. paratuberculosis, that is unable to grow under specific conditions. It is especially useful for identifying loci involved in pathogenicity. It is useful in constructing vaccines. The method can be used to screen conditiple libraries concurrently. It can screen libraries of different organisms or different strains of the same organism. The present protein is encoded by a gene which is disrupted by the insertion of the IS 1096 transposon to produce an attenuated mutant of Mycobacterium tuberculosis
                                                                   Query Match
Best Local S
Matches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Screening a mutant library for mutants unable to grow under specific conditions and for identifying loci involved in pathogenicity, comprises using signature tagged transposon mutagenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mycobacterium tuberculosis; attenuated microorganism; mmpL7; Rv2942; signature tagged transposon mutant; mutant library; mycobacterial infection; actinomycetales; antibacterial; immunostimulant;
                                                                                                                                                                                                                                                                                                                                                                                                                     library with insertions in genes and/or regulatory regions of the organisms of interest, where the insertion contains a tag and/or a transposon associated with a tag. The mutants are identified by hybridisation of the tags to known sequences. The method is useful for hybridisation of the tags to known sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gicquel B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-JUL-1999;
08-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is given in a specification relating to a method screening a library of mutants. The method comprises constructing a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 8; Fig 14A; 159pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-JUL-2000; 2000WO-IB000950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200102555-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein encoded by Mycobacterium tuberculosis mmpL7 (Rv2942)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB66456;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB66456 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-JAN-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (INSP ) INST PASTEUR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2001-091804/10.
)B; AAF31617.
876
                                                                   10;
                                  N
                                                                                      Similarity
                                                                                                                                       920
FGAGLVLVSGGSF 888
                                FGAGLVL--GGQF 12
                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Guilhot C,
                                                                                                                                       ξ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0142982P
99US-0142833P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entry)
                                                                                    61.2%;
76.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Camacho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            920 AA
                                                                 Score 41; DB
Pred. No. 6e+0
0; Mismatches
                                                                   0;
                                                                                    DB 4;
6e+02;
                                                                                                  Length 920;
                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mmpL7; Rv2942;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene
                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for
                                                                                                                                                                                                                                                                                 18
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RESULT 14

Propionibacterium acnes

dermatological; osteopathic; neuroprotectant

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AAU51976
ID AAU5
XX
AC AAU5
XX
AC AAU5
XX
DT 27-F
XX
DE Prop
XX
XX
DE Prop
XX
VX
VX
Uvel
XM
Uvel
XM
Uvel
XM
Uvel
XM
OB Prop
XX
OS Prop
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                                                                                                                                                                                                                                    RESULT 15
                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is transmembrane transport protein MMPL7. It is encoded by a gene which is down-regulated during survival under carbon starvation and oxygen limitation conditions. The specification describes mycobacterial genes which are down-regulated during a stationary phase culture of mycobacteria under nutrient-starving culture conditions, when compared with an exponential phase culture of mycobacteria under culture conditions that are not nutrient-starving and that support exponential growth of the mycobacteria. Mycobacterial polypeptides which are down-regulated under nutrient-starving conditions are useful for the manufacture of a medicament for treating or preventing a mycobacterial infection. They may also be useful as vaccines
                                           SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated mycobacterial peptides, useful for the manufacture medicament for treating or preventing a mycobacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jameв ВW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mycobacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleotide sequence of gene down-regulated during nutrient starvation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABR55195 standard;
                                                                                                         Propionibacterium acnes immunogenic protein #12872.
                                                                                                                                         27-FEB-2002
                                                                                                                                                                      AAU51976;
                                                                                                                                                                                                     AAU51976 standard;
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 920 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; ACC43891.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MICR-) MICROBIOLOGICAL RES AUTHORITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-OCT-2001; 2001GB-00025535.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-OCT-2002; 2002WO-GB004718.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO2003035681-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Carbon starvation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-JUL-2003
                                                                                                                                                                                                                                                                                 876 FGAGLVLVSGGSF 888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2003-421402/39.
                                                                                                                                                                                                                                                                                                            2 FGAGLVL--GGQF 12
                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Page 117-121; 138pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Marsh P,
                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        infection; transmembrane transport protein MMPL7
                                                                                                                                                                                                     protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nutrient-starving culture; mycobacteria; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein; 920
                                                                                                                                                                                                                                                                                                                                                           61.2%;
76.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hampshire
                                                                                                                                                                                                     57
                                                                                                                                                                                                                                                                                                                                           Score 41; DB
Pred. No. 6e+0
0; Mismatches
                                                                                                                                                                                                                                                                                                                                              0
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                                                                                                                                                                                                                                                                                                                                                             6e+02;
                                                                                                                                                                                                                                                                                                                                                                           DB 6;
                                                                                                                                                                                                                                                                                                                                                                          Length 920
                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                             2;
                                                                                                                                                                                                                                                                                                                                              Gaps
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RESULT 16
ABM48495
ID ABM48
XX ABM48
AC ABM48
XX 20-OC
DT 20-OC
XX YOU
DE Propi
XX Acne
XW immur
XX Propi
XX Propi
XX WO20(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     뭐
                                                                                                                                                                                                                                                                                                                                                          S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pustulosis, hypertosis and osteomyelitis), weitts and endophthalnitis.

CP. acnes is also involved in infections of bone, joints and the central CP. acnes is also involved in infections of bone, joints and the central CP. acnes is sparticularly involved in the inflammatory construction associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a compression of a binding agent that binds to the proteins of the invention of and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as characteristic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA). Note: The sequence data for obtained in electronic format directly from WIPO at Cpub/pub/pub/lished per sequence.
                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                Propionibacterium acnes predicted ORF-encoded polypeptide #13171
WO2003033515-A1
                                                                                                                                                             20-OCT-2003
                                                                                                                                                                                                                               ABM48495 standard; protein; 57
                                 Propion1bacterium
                                                                                                                                                                                                 ABM48495,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 57 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
                                                                              Acne vulgaris; antiseborrhoeic; dermatological; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; SEQ ID NO 13171; 1069pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Propionibacterium acnes vaccinating against and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-APR-2000; 2000US-0199047P.
02-JUN-2000; 2000US-0208841P.
07-JUL-2000; 2000US-0216747P.
                                                                   mmunostimulant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  treating acne vulgaris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-616774/71.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Skeiky YAW, Persing DH, L'maisonneuve J, Zhang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-APR-2001; 2001WO-US012865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200181581-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
les 8; Conserv
                                                                                                                                                                                                                                                                                                                          43
                                                                                                                                                                                                                                                                                                                                                           N
                                                                                                                                                                                                                                                                                                                                                        FGAGLVLGGQ 11
                                                                                                                                                                                                                                                                                                                        FGAGLVYAGQ 52
                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                          (first entry)
                                                               immune response; vaccine
                                 acnes
                                                                                                                                                                                                                                                                                                                                                                                                            59.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polypeptides and nucleic acids useful for diagnosing infections, especially useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mitcham JL, Wang SS, Jen S, Carter D;
                                                                                                                                                                                                                                                                                                                                                                                          Score 40; DB
Pred. No. 47;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                           0,
                                                                                                                                                                                                                                                                                                                                                                                                                           4; Length 57
                                                                                                                                                                                                                                                                                                                                                                                          2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bhatia A;
                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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ABO83978
ID ABO8
XX
AC ABO8
XX
AC ABO8
XX
DT 29-J
XX
DE Pseu
XX
KW Bact
                                                                                                                                                                                                                                RESULT 17
                                                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                                                                 δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CC rhe invention relates to an isolated polynucleotide (ACF64435-ACF64733)
CC encoding a Propionibacterium acnes protein. The invention also relates to polypeptides encoded by the polynucleotides (ABM35624-ABM64336) and to CC polypeptides encoded by the polynucleotides. The invention and to CC immunogenic fragments of P. acnes polypeptides. The invention additionally encompasses expression vectors and host cells comprising a CC polynucleotide of the invention; antibodies against polypeptides of the cinvention; a composition of the invention; a composition of comprising P calls prepared composition (comprising P calls prepared composition (comprising P calls prepared complete the composition of the polynucleotides, and a composition of comprising P cacnes polypeptides, complete the polypeptides, or composition of the polynucleotides and kit composition of the cacnes in a complete composition of the cacnes in a composition of the cacnes of P. acnes in a complete composition of the cacnes of proteins, T cell populations or antigen-presenting cells that express the colypeptides are useful for diagnosing, preventing or treating acnes composition. The polynucleotides can also be used as probes or primers for complete caches and the caches proteins. The caches can also be used as probes or primers for complete caches and the kit is useful for performing a diagnostic assay. The present composition is useful for the caches composition is useful for the caches composition assay. The present composition is useful for the present of the printed specification, but was obtained in electronic format directly form mart of the printed specification, but was obtained in electronic format directly composition in the present of the composition in the present of the composition in the present of the composition 
                                                                                                                                                                                                                                                                                                                                                                               Matches
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Best Local (
                                                         Pseudomonas aeruginosa polypeptide #16153.
                                                                                                     29-JUL-2004
                                                                                                                                               AB083978;
                                                                                                                                                                                  ABO83978 standard; protein; 171 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 57 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New Propionibacterium acnes polypeptides and polynucleotides encoding the polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; SEQ ID NO 13171; 1481pp; English.
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N-PSDB; ACF64482.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mitcham JL, Skeiky YAW, Pers
Zhang Y, Wang S, Jen S, Lod
Barth B, Vallieve-Douglass J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-OCT-2002; 2002WO-US032727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-OCT-2001; 2001US-00978825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CORI-) CORIXA CORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-APR-2003
                                                                                                                                                                                                                                                                                              43
                                                                                                                                                                                                                                                                                                                                     N
                                                                                                                                                                                                                                                                                                                                                                           Similarity 80.08; Conservative
                                                                                                                                                                                                                                                                                            FGAGLVYAGO
                                                                                                                                                                                                                                                                                                                                 FGAGLVLGGQ 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Skeiky YAW,
ang S, Jen S,
                                                                                                   (first entry
                                                                                                                                                                                                                                                                                            52
                                                                                                                                                                                                                                                                                                                                                                                               59.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Persing DH,
Lodes MJ,
                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                 Score 40; DB
Pred. No. 47;
                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bhatia A,
Benson DR,
                                                                                                                                                                                                                                                                                                                                                                                                                  6
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                                                                                                                                                                                                                                                                                                                                                                                                                Length 57;
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Jones R, Carter D;
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Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.

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RESULT 18
ABM65541
ID ABM65
XX ABM65
XX ABM65
XX ABM65
XX ACOC
DT 20-OC
DT 20-OC
DT ACOC
DT 20-OC
DT 20-OC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CC The invention relates to Pseudomonas aeruginosa polypeptides and the CC polynucleotides encoding them. The sequences are useful in diagnosis and CC therapy of pathological conditions, as molecular targets for diagnostics, CC prophylaxis and treatment of pathological conditions resulting from a CC bacterial infection, for evaluating a compound, such as a polypeptide, CC for the ability to bind a P. aeruginosa nucleic acid, as components of CC effective antibacterial targets, as targets for antibacterial drugs, CC including anti-P. aeruginosa drugs, as templates for recombinant CC production of P. aeruginosa-derived peptides or polypeptides, as target CC components for diagnosis and/or treatment of P. aeruginosa-caused CC infection, and in detection of P. aeruginosa sequences or ther sequences of Pseudomonas species using biochip technology. Sequences ABO67826-CC ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed CC specification but was obtained in electronic format from USPTO at Sequence.
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                                 11-OCT-2002; 2002WO-US032727
                                                                                               24-APR-2003.
                                                                                                                                                                                                                                                                                                                                                                              Propionibacterium acnes immunogenic polypeptide #30217
                                                                                                                                                                                                                                                                                                                                                                                                                                             20-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABM65541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABM65541 standard; protein; 406 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 171 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 32724; 455pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; ABD17549.
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27-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pseudomonas aeruginosa.
                                                                                                                                                                                                                      Propionibacterium
                                                                                                                                                                                                                                                                                  immunostimulant; immune response; vaccine; immunogenic
                                                                                                                                                                                                                                                                                                                   Acne vulgaris; antiseborrhoeic; dermatological; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rubenfield MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GENO-) GENOME THERAPEUTICS CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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98US-0094190P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59.7%;
77.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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ABB61739
ID ABB6
XX ABB6
XX 26-M
XX Dros
XX Dros
KW Dros
KW Dros
KW Dhai
XX Dros
KW Dhai
XX WO2(
XX Dros
27-4

27-SEP-2001

WO200171042-A2

Drosophila melanogaster

Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.

Drosophila melanogaster polypeptide SEQ ID NO 12009

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392

FGAGLVYAGQ 401

2 FGAGLVLGGQ 11

Matches

Conservative

<u>.</u>.

Indels

<u>.</u>

Gaps

0

RESULT 19

ABB61739;

ABB61739 standard;

protein;

805

26-MAR-2002

(first entry)

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The invention relates to an isolated polynucleotide (ACF64435-ACF64733) CC encoding a Propionibacterium acnes protein. The invention also relates to computation and to immunogenic fragments of p. acnes polypeptides. The invention computation and thodies against polypeptides of the invention, antibodies against polypeptides of the invention; a method for stimulating an immune response specific for a p. acnes polypeptide and an isolated T cell population comprising P. acnes polypeptides, completely antipodies, fusion proteins, T cell populations, or computation comprising P. acnes polypeptides, comparison proteins, T cell populations, or contain an method for inhibiting the development of P. acnes in a patient; and a method for inhibiting the development of P. acnes in a composition comprising proteins, or composition of proteins, T cell populations or antigen-presenting cells that express the polypeptides, antibodies, fusion proteins, or for stimulations or antigen-presenting creates the patient, and a method for inhibiting the development of P. acnes in a patient, and a method for inhibiting the development of P. acnes in a composition, and the composition of an immune response specific for a p. acnes the polypeptides are useful for diagnosing, preventing or treating acnes composition, in the polyment of an immune response against P. acnes, or for treating acne, and the kit is useful for performing a diagnostic assay. The present composition is useful for the printed specification, but was contain an immunogenic region. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                      Query Match
Best Local
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Zhang Y, Wa
Barth B, Va
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New Propionibacterium acnes polypeptides and polynucleotides encoding the polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein.
                                                                                             Sequence 406 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-OCT-2001; 2001US-00978825.
                                                                                                                                         ftp.wipo.int/pub/published_pct_sequences
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Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 30217; 1481pp; English.
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Vallieve-Douglass J;
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ng S, Jen S,
                      59.7%;
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Score 40; DB Pred. No. 3.7e.
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Benson DR,
                                                 DB 6;
                        .7e+02;
                                            Length 406;
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Jones R, Carter D;
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ARESULT 20
ADJ69760
ID ADJ69760
ADJ69760
ADJ697
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Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB018737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly the sequences of the sequence data for this patent did not format directly appropriate of the sequence data for this patent did not format directly the sequence data for this patent did not format directly the sequence data for this patent did not format directly the sequence data for this patent did not format directly the sequence data for this patent did not format directly the sequence data for this patent did not format directly the sequence data for this patent did not format directly the sequence data for this patent did not format directly the sequence data for this patent did not format directly the sequence data for this patent did not format directly the sequence data for this patent did not format directly the sequence data for this patent did not format directly the sequence data for the sequence data for this patent did not format directly the sequence data for the sequence data for this patent did not format directly the sequence data for this patent did not format directly the sequence data for this patent did not format directly the sequence data for the sequence dat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mitochondrial; human; screening assay; diabetes mellitus; Huntington's disease; osteoarthritis; Leber's hereditary optic neuropathy; LHON; mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated nucleic a
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11-JUL-2000;
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                                                                                                     12-APR-2002; 2002US-0372843P.
17-JUN-2002; 2002US-0389987P.
20-SEP-2002; 2002US-0412418P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         myoclonic epilepsy ragged red fibre syndrome; neuroprotective; nootropic; antidiabetic; anti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 805
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                                                                                                                                                                                                                                          04-APR-2003; 2003WO-US010870
                                                                                                                                                                                                                                                                                                                                                                                       WO2003087768-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human heat mitochondrial protein as a therapeutic target SeqID1566
(MITO-)
                                                                                                                                                                                                                                                                                                                  23-OCT-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            osteopathic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADJ69760 standard;
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                                    MITOKOR
   BUCK INST AGE RES.
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2000US-00614150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ophthalmological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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a and
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54.5%;
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Pred. No. 7.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cytostatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Myers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MERRF;
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and cell-cell
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Best Local S
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25-MAR-1997;
14-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for therapeutic intervention in treating a disease associated with altered mitochondrial function. Specifically, it refers to a method for identifying proteins of the human heart mitochondrial proteome that are useful for drug screening assays, as well as therapeutic targets. The present invention describes a method for identifying such proteins that can be used in the treatment of various diseases associated with altered mitochondrial function including diabetes mellitus, Huntington's disease, osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Identifying a mitochondrial target for drug screening assays and for treating diseases associated with altered mitochondrial function, comprises detecting a modified polypeptide in a sample and correlating with the disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ghosh SS,
Warnock DE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ragged red fibre syndrome (MERRF) or cancer. Accordingly, these compositions have neuroprotective, nootropic, antidiabetic, antiarthritic to soteopathic, ophthalmological and cytostatic activities. This polypeptide sequence is a human heart mitochondrial protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 875 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This
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                                                      N-PSDB; AAX30556
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Helicobacter pylori.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cytoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vaccine; probe;
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                                                                                                                               Smith D,
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97US-00823745.
97US-00891928.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diagnostic; ORF; cell envelope protein; secreted
tein; cellular protein.
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                                                                                                                                    Kabok
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New isolated Helicobacter pylori nucleic

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Matches 7
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24-JUN-1997;
29-JUL-1997;
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This sequence represents a Helicobacter pylori GHPO protein of the invention. The polypeptides can be used for preventing or treating Helicobacter infections, and gastroduodenal diseases associated with these infections, including acute, chronic, and atrophic gastritis, and peptic ulcer diseases, e.g. gastric and duodenal ulcers. They can also be used for the production of antibodies. The products can also be used for
                                                                                                                                                                                                                                                    New isolated Helicobacter polynucleotides - used to develop products for the diagnosis, prevention and treatment of Helicobacter infections and gastrointestinal diseases.
                                                                                                                                                                                               Claim 8; Page 111-113; 2054pp; English.
                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1998-542293/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GHPO protein;
peptic ulcer (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kleanthous H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pylori GHPO 635 protein.
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er Helicobacter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 GAGLVLGGQFM 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MERIEUX ORAVAX PASTEUR MERIEUX SERUMS HUMAN GENOME SCI INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    disease
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97US-00881227.
97US-00902615.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Helicobacter infection; gastroduodenal disease; gastritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Page 190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Al-Garawi A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98WO-US006371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prevention and treatment of infection by \mathbf{H}_{\cdot} pylori and species.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein; 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     339pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pure preparations of H. pylori polypeptides the nucleic acids encoding them. In all, 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Miller C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 39;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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2.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tomb J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oomen
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ABU22234 ID ABU XX

ABU22234

standard;

protein;

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RESULT 24

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Matches 7
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Matches
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                                                                                                            The invention relates to a vaccine for preventing or treating infections by Helicobacter pylori. The vaccine contains at least one isolated H. pylori polypeptide, or its fragments, in a carrier, where the carrier is a Salmonella, Vibrio cholerae or Shigella vector containing a nucleic acid encoding the H. pylori polypeptide. The vaccines induce humoral and cellular immune responses. The vaccines are used to treat or prevent infections by H. pylori. Sequences AAX75779 to AAX75837 represent nucleic acid sequences encoding H. pylori outer membrane polypeptides (OMPB)
                                                                                 Sequence 220 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Outer membrane polypeptide; OMP; vaccine; H. pylori infection; humoral; cellular immune response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 H. pylori outer membrane polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY17195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 220 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            detection and diagnosis
                                                                                                                                                                                                             Claim 7;
                                                                                                                                                                                                                                  Cellular vaccine against Helicobacter
                                                                                                                                                                                                                                                        N-PSDB; AAX75814
                                                                                                                                                                                                                                                                  WPI; 1999-326698/27
                                                                                                                                                                                                                                                                                        Ellis
                                                                                                                                                                                                                                                                                                                                  28-OCT-1997;
17-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                 28-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                     06-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                             Helicobacter pylori
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY17195
                                                                                                      AAY17160
                                                                                                                                                                                                                                                                                                                                                                                                         WO9921959-A2
                                                                                                                                                                                                                                                                                                             (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
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                                      Similarity 7; Conserv
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               GAGLVLGGQFM 13
                                                                                                                                                                                                             Page 269-270; 352pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GFGVVLGGKFV 80
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GFGVVLGGKFV
                                                                                                      to AAY17218
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                                         Conservative
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97US-00993001.
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                                                                                                                                                                                                                                                                                        BM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein;
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                                                  58.2%;
80
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                                        Score 39; DB
Pred. No. 2.8e
3; Mismatches
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Pred. No. 2.8e+02;
                                                                                                                                                                                                                                                                                        Smith
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                                                                                                                                                                                                                                  pylori.
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                                                   .8e+02;
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ABU22234;

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CC The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression CC (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense CC nucleic acid; (2) a host cell containing the vector; (3) an isolated CC polypeptide or its fragment whose expression is inhibited by the antisense CC nucleic acid; (4) an antibody capable of specifically binding CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular CC proliferation or the activity of a gene in an operon required for proliferation, or that has an activity against a biological pathway in which a proliferation, or that inhibits cellular proliferation; (8) identifying a compound that influences the activity of cor a gene on which the test compound that inhibits proliferation of a proliferation or the proliferation or the proliferation or the proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a CC compound's activity; (11) a culture comprising strains in which the gene product is overexpressed of 1(12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for cellular proliferation of an organism. The antisense nucleic acids are useful for cellular proliferation in cells other than S. aureus, S. typhimurium, CC the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained cc in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wang L,
Wall D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-MAR-2001; 2001US-00815242.

06-SEP-2001; 2001US-00948993.

25-OCT-2001; 2001US-0342923P.

08-FEB-2002; 2002US-00072851.

06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-OCT-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antisense; prokaryotic essential gene; cell proliferation; drug design
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein encoded by Prokaryotic essential gene #7761.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-MAR-2002; 2002WO-US009107.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ELIT-)
                                      ftp.wipo.int/pub/published_pct_sequences
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Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 50158; 1766pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Malone C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Haselbeck R, Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ohlsen
Forsyth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ₽ <u>₹</u>
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Xu HH;
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Query Match
Best Local Similarity
Matches 8; Conserv

Conservative

58.2%;

Score 39; DB 6; Pred. No. 5.5e+02; 2; Mismatches 3

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Gaps

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RESULT 26
ABR53218
ID ABR53
XX

ABR53218 standard; protein; 770 AA.

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Length 419; Indels

Sequence 419 AA;

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RESULT 25
ADE86082
ID ADE86
XX Claim
XX
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                                                                                                                                                                                                                                                                               The present sequence is the protein sequence of an efflux protein thought to be involved in the biosynthesis of the peptide antibiotic AC98 of CC Streptomyces hygroscopicus NS17 (NRRL 30439). The sequence is predicted CC from an open reading frame (ORP10) in a gene cluster ADE86070 isolated CC complex. Sequence comparisons of specific ORFs indicated that the encoded CC complex. Sequence comparisons of specific ORFs indicated that the encoded CC proteins are tailoring enzymes involved in modification of the AC98 CC peptide core, e.g. glycosylation, methylation or acylation, or in CC transformed host cells. It also provides a method of producing acyclic CC peptide antibiotic, such as AC98, using the NRPS comprised of mppA CC lipoglycopeptide antibiotic with activity against Gram-positive CC pathogens. Also provided are methods of modifying NRPS to produce an CC antibiotic having a modified peptide core, and a method for evaluating CC the structural regions of the modified peptide.
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                                                                                                                    Matches
                                                                                                                                                 Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADE86082 standard; protein; 450 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-812536/76.
N-PSDB; ADE86070.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 10; SEQ ID NO 30; 163pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New non-ribosomal peptide synthetase, useful for preparing antibacterial peptides, derived from Streptomyces, also related nucleic acid and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hucul JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (AMHP ) WYETH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-MAR-2002; 2002US-0368713P
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                                                                                                                                                                                                                                        Sequence
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305 FGAGGLLGGLF 315
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                                                          2 FGAGLVLGGQF 12
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                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                           450 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antibiotics.
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                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                    58.2%;
72.7%;
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                                                                                                                                                    Score 39; DB 7;
Pred. No. 5.9e+02;
                                                                                                                          Mismatches
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RESULT 27
ADK63726
ID ADK63726
AC ADK63
XX O6-MB
DT O6-MB
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OS Unide
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Matches 7
                                                                                                                                                                                                                                                                                                                                                            ABR52568-ABR53903 and ACC60610-ACC61944 respectively. The complexes are obtainable by using a protein as a balt and isolating the set of proteins which is attached thereto from cells. Such protein complexes are up to 30 distinct proteins. Protein complexes or disprise of the invention are useful for diagnosing a disease or disorder, or as a target for an active agent of a pharmaceutical, preferably a drug target in the treatment or prevention of a disease or disorder. Note: The sequence data for this patent is not represented in the printed specification, but is based on sequence information supplied by the European Patent Office. The complete document is available on CD-ROM
                                                                                                                   06-MAY-2004
                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 1301; 17pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  disorder, or as a target for an active agent of a pharmaceutical, preferably a drug target in the treatment or prevention of disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bauer A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saccharomyces cerevisiae
             EP1338608-A2
                                       Unidentified
                                                                                         Disease treating protein complex-derived protein #790
                                                                                                                                             ADK63726;
                                                                                                                                                                       ADK63726 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated protein complexes useful for diagnosing a disease or disorder, or as a target for an active agent of a pharmaceutical,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; ACC61260.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-DEC-2001; 2001EP-00130253
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                                                                                                                                                                                                                                        142
                                                                                                                                                                                                                                                               2 FGAGLVLGGQ 11
                                                                                                                                                                                                                                                                                          Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence #SEQ ID 1301.
                                                               complex;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CELLZOME AG
                                                                                                                                                                                                                                                                                                                                             770
                                                                                                                                                                                                                                       | ||||:||:
| FSAGLVIGGK 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gavin A, Grand
M, Schultz JD,
                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    relates to multiprotein complexes from eukaryotes.
                                                               drug
                                                                                                                                                                      protein; 770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Grandi P,
                                                                                                                                                                                                                                                                                                     58.2%;
70.0%;
                                                               target; diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Superti-Furga GD;
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                                                                                                                                                                                                                                                                                                      Score 39;
Pred. No.
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                                                                                                                                                                       ₽
                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                      1e+03;
                                                                                                                                                                                                                                                                                                                  DB 6;
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                                                                                                                                                                                                                                                                                                                  Length 770;
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RESULT 28
ABJ26177
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Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        second protein, or its derivative, fragment, homologue or variant. The proteins are selected from given protein complexes, which are not defined in the specification. The variants are encoded by nucleic acids that conditions. The protein complexes are useful as care to the mucleic acids encoding the proteins under low stringency conditions. The protein complexes are useful as targets for an active agent of a pharmaceutical. These protein complexes are particularly useful as drugs targets for the treatment or preventing of a disease or disorder. The complexes and methods above are useful in diagnosing or screening for the presence of a disease or disorder or a predisposition for developing a disease or disorder in a subject. These are also useful in screening for a drug for treatment or prevention of a disease or disorder. The molecule that modulates the amount, activity or protein components of the complex is useful for the manufacture of a medicament for the treatment or prevention of disorder. This sequence corresponds to a protein of the invention. (Note: the sequence data for this patent did not form part of the printed specification but was obtained from the EPO in electronic format).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New proteins and protein complexes from eukaryotes, useful as targets drug screening, or in diagnosing or screening for the presence of a disease or disorder, or a predisposition for developing a disease or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Marzioch M, Grann-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 770 AA;
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                                                                                                                                                                                                                                                                                                 ABJ26177;
                                                                                                                                                                                                                                                                                                                                   ABJ26177 standard; protein; 810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to novel protein complexes comprising a first and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 1579; 13pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     disorder in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-DEC-2001; 2001EP-00130253
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M, Grandi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a subject.
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                                                                                                                                                                                                                                                           (first entry)
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i P, Krause R,
n C, Rick J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58.2%;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 7;
1e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <u>,</u>
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Fungicide; cytostatic; essential gene; Aspergillus fumigatus; infection; cancer; contamination; biofilm; antibody; immune response.

23-APR-2002; 2002WO-US013142

31-OCT-2002

Aspergillus fumigatus

Aspergillus

fumigatus essential

gene protein #835

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consider (e.g. cancer), to prevent or contain containation of an object by A. fumigatus, or to prevent or inhibit formation on a surface of a contain comprising A. fumigatus. The polynucleotides are useful for cexpressing recombinant protein for characterisation, screening or comparism throat or comparing with the pathogenic corganisms invade or reside, for comparing with the DNA sequence of A. CC fumigatus to identify duplicated genes or paralogues having the same or funiquatus to identify duplicated genes or paralogues having the same or similar biochemical activity and/or function, for comparing with DNA sequences of other related or distant pathogenic organisms to identify potential orthologous essential or virulence genes, for selecting and comparing of comparing organisms to identify making oligomers for attachment to a nucleic acid array for examination of expression patterns, for raising anti-protein antibodies, as an conference of expression patterns, for raising anti-protein antibodies, as an expression patterns, for raising anti-protein antibodies, as an conference of elicit immune response, as a reagent in assays designed to quantitatively conference of the protein of the binding cours or to identify inhibitors of the activation of the binding cours or to identify inhibitors of the activation of the binding cours or to identify inhibitors of the activation of the binding cours or to identify inhibitors of the activation of the binding cours or to identify inhibitors of the activation of the protein in biological fluids, as a marker for host risenes in which hardwards or variation and to contain a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-APR-2001; 2001US-0285697P.
27-APR-2001; 2001US-0287066P.
05-UNN-2001; 2001US-0295890P.
09-UTL-2001; 2001US-0303899P.
31-AUG-2001; 2001US-0316362P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the invention a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to novel purified or isolated nucleic essential genes of Aspergillus fumigatus. The isolated nucle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page; 175pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ELIT-)
                                                                                                            Fungicide; cytostatic;
cancer; contamination;
                                                                                                                                                                             Aspergillus fumigatus essential gene protein #235.
                                                                                                                                                                                                                             16-APR-2003
                                                                                                                                                                                                                                                                                                                        ABJ25577 standard; protein; 811 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    host tissues in which pathogenic organism invade or reside, and to isolate correlative receptors or ligands in the case or virulence factors. This sequence represents a protein of one of the essential genes of Aspergillus fumigatus of the invention
                     WO200286090-A2
                                                                Aspergillus fumigatus
                                                                                                                                                                                                                                                                                                                                                                                                                                         148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                       FSAGLVIGGK 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FGAGLVLGGQ 11
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A
                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zamudio
                                                                                                                essential gene; Asp
biofilm; antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 39; DB
Pred. No. 1.1e
2; Mismatches
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1;
                                                                                                                                      Aspergillus fumigatus; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 6; Length 810;
                                                                                                                   immune
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                                                                                                                   response
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ABO76231
ID ABO
XX ABO
AC ABO
DX 29XX 29XX Pse
XX Bac
XX Bac
XX Pse

Pseudomonas 29-JUL-2004

aeruginosa polypeptide #8406.

(first entry

Bacterial infection; Pseudomonas aeruginosa infection; antibacterial

Pseudomonas aeruginosa

밁 8

148

FSAGLVIGGK 157

2 FGAGLVLGGQ 11

0

RESULT 30

ABO76231 standard;

protein; 903

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CC by A. funigatus, or to prevent or inhibit formation on a surface of a CC by A. funigatus, or to prevent or inhibit formation on a surface of a CC by A. funigatus. The polymucleotides are useful for CC expressing recombinant protein for characterisation, screening or CC therapeutic use, as markers for host tissues in which the pathogenic CC quantisms invade or reside, for comparing with the DNA sequence of A. CC similar blochemical activity and/or function, for comparing with DNA CC similar blochemical activity and/or function, for comparing with DNA CC sequences of other related or distant pathogenic organisms to identify CC potential orthologous essential or virulence genes, for selecting and CC making oligomers for attachment to a nucleic acid array for examination of expression patterns, for raising anti-protein antibodies, as an CC antigen to raise anti-DNA antibodies or to elicit another immune casponse, and for identifying polymucleotides encoding the other protein contraction. The polypeptides may be used to raise antibodies or to elicit immune response, as a reagent in assays designed to quantitatively determine levels of the protein in biological fluids, as a marker for CC determine levels of the protein in biological fluids, as a marker for CC isolate correlative receptors or ligands in trace as a marker for of Aspergillus fumigatus of the invention
  Matches
                     Query Match
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27-APR-2001; 2001US-0287066P.
05-JUN-2001; 2001US-0295890P.
09-JUL-2001; 2001US-0303899P.
31-AUG-2001; 2001US-0316362P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to novel purified or isolated nucleic acids of essential genes of Aspergillus fumigatus. The isolated nucleic acids the invention are used to treat or prevent infections by a pathogenic organism such as A. fumigatus, to treat a non-infectious disease in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New purified or isolated nucleic acids of essential genes of Aspergillus fumigatus, useful for treating or preventing infections by A. fumigatus, or for treating a non-infectious disease in a subject e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-APR-2002; 2002WO-US013142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        subject (e.g. cancer), to prevent or contain contamination of an object by A. fumigatus, or to prevent or inhibit formation on a surface of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page; 175pp; English.
                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2003-093124/08
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Similarity 7; Conserve
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                                                                                    811 AA;
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    Conservative
                       58.2%;
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                     Score 39;
Pred. No. 1
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        Mismatches
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                       1.1e+03;
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                                               Length 811;
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ARESULT 31
AAG35239
ID AAG35
XX AAG35
AC AAG35
XX DT 18-OX
XX Prott
KW Prott
KW Prott
KW hybr:
XX Lermi
XX Ermi
XX EP10:
XX EP10:
XX X EP10:
XX Y EP10:
XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to Pseudomonas aeruginosa polypeptides and the CC polynucleotides encoding them. The sequences are useful in diagnosts and CC therapy of pathological conditions, as molecular targets for diagnostics, CC prophylaxis and treatment of pathological conditions resulting from a CC batterial infection, for evaluating a compound, such as a polypeptide, CC for the ability to bind a P. aeruginosa nucleic acid, as components of CC effective antibacterial targets, as targets for antibacterial drugs, CC including anti-P. aeruginosa drugs, as templates for recombinant CC production of P. aeruginosa drugs, as templates for recombinant CC infection, and in detection of P. aeruginosa sequences or other sequences CC infection, and in detection of P. aeruginosa sequences or other sequences CC feducation, by a companion of P. aeruginosa sequences ABO67826.

CC ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed CC septents users obtained in electronic format from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection.
                    25-FEB-2000; 2000EP-00301439
                                                                                                                                                           Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence; corn.
                                                                                                                                                                                                                                Zea mays protein fragment SEQ ID NO: 43019.
                                                                                                                                                                                                                                                                                                                                           AAG35239 standard; protein; 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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27-JUL-1998;
                                                        06-SEP-2000.
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9; Conserv
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98US-0094190P.
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Pred. No. 1.5e+03;
1; Mismatches 1
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05-MAY-1999,
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99US-0123548P.
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99US-0126264P.
99US-0126785P.
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3-0143542P. 5-0143624P. 5-0144005P.

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RAG35231
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23-MAR-1999
25-MAR-1999
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14-0CT-1999
121-0CT-1999
21-0CT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence; corn.
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99US-0158029P

99US-0158332P

99US-0159293P

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99US-0159330P

99US-0159331P

99US-0159337P

99US-0159537P

99US-0169637P

99US-0160764P

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99US-0160789P

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S-0146386P S-014738PP S-0147738P S-0147738P S-0147726PP S-014716P S-014716P S-0147339P S-0147339P S-0148319P S-014834PP S-0148368PP S-0149175P S-01510864P S-0151086P S-0151088P S-015139P S-0155486P S-0156458P S-0156458P

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99US-0132048P 99US-0132487P 99US-0132487P 99US-0132487P 99US-0134256P 99US-0134221P 99US-0134221P 99US-0134221P 99US-0134221P 99US-0134221P 99US-0134221P 99US-0134221P 99US-0134241P 99US-0134241P 99US-013424P 99US-013424P 99US-013629P 99US-013629P 99US-013629P 99US-013629P 99US-013629P 99US-013945P 99US-013945P 99US-013945P 99US-013945P 99US-013945P 99US-013945P 99US-013945P 99US-013945P 99US-013945P 99US-013945P 99US-013945P 99US-013945P 99US-014055P 99US-014264P 99US-014364P 99US-014364P 99US-014364P 99US-014364P 99US-014364P 99US-014365P 99US-014335P 99US-0144335P	99US-0128234P. 99US-0128714P. 99US-0129845P. 99US-0130077P. 99US-0130449P. 99US-0130510P. 99US-0130840P.
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RESULT 33
AAG440537
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09-MAR-1999;

23-MAR-1999;

25-MAR-1999;

25-MAR-1999;

01-APR-1999;

06-APR-1999;

16-APR-1999;

16-APR-1999;

19-APR-1999;

21-APR-1999;

21-APR-1999;

23-APR-1999;

23-APR-1999;
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hybridisation assay; genetic mapping; gene expression control; promoter;
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Similarity 66.7%;
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99US-0159329P.
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99US-012548P.
99US-0125788P.
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99US-0127462P.
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99US-0128234P.
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99US-01300510P.
99US-0130891P.
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Pred. No. 3.5e+02;
2; Mismatches 1; Indels
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99US-0134221P.
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99US-0134221P.
99US-0135528P.
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RESULT 34

AAG04531

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Similarity 66.7%;
6; Conservative
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        99US-0121825P.
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99US-0130049P.
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Pred. No. 3.7e
2; Mismatches
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3.7e+02;
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99US-0149929P. 99US-0149902P. 99US-0149902P. 99US-0150884P. 99US-0151086P. 99US-0151080P. 99US-01513758P. 99US-0153758P. 99US-0154779P. 99US-0155459P. 99US-0155659P. 99US-0156586P. 99US-015865P. 99US-0158232P. 99US-0158233P. 99US-0158233P. 99US-0158233P. 99US-0158233P. 99US-0158233P. 99US-0159293P. 99US-0159330P. 99US-0159331P.	

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09-MAR-1999
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21-APR-1999
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                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana
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llarity 66.7%;
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99US-0121825P

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99US-0125788P

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99US-0161361P.
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99US-0161932P.
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Pred. No. 3.7e+02;
2; Mismatches 1
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21-MAY-1999

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26-OCT-199;
28-OCT-1999;
28-OCT-1999;
28-OCT-1999;
29-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana.
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2 FGCGVILGG 140
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ilarity 66.7%;
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99US-01301449P.
99US-0131449P.
99US-0132484P.
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99US-0132484P.
99US-0132484P.
99US-013421P.
99US-013421P.
99US-013421P.
99US-013431P.
99US-013431P.
99US-013431P.
99US-0135353P.
99US-013623P.
99US-013623P.
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99US-0161361P.
99US-0161920P.
99US-0161992P.
99US-0161993P.
99US-0162142P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entry)
                                                                                                                                                                                                                                                                                                                                                                                                                             signal transduction pathway;
netic mapping; gene expression
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4.6e+02;
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on control;
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28-JUL-1999
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20-AUG-1999 23-AUG-1999 24-AUG-1999 25-AUG-1999 27-AUG-1999 28-SEP-1999 28-SEP-1999 29-SEP-1999 20-SEP-1999 20-SEP-1999 21-OCT-1999 22-OCT-1999 23-SEP-1999 24-OCT-1999 25-OCT-1999 26-OCT-1999 27-OCT-1999 28-OCT-1999	5-AUG-1999; 5-AUG-1999; 6-AUG-1999; 6-AUG-1999; 9-AUG-1999; 9-AUG-1999; 1-AUG-1999; 1-AUG-1999; 1-AUG-1999; 1-AUG-1999; 1-AUG-1999; 1-AUG-1999; 1-AUG-1999; 1-AUG-1999; 1-AUG-1999; 1-AUG-1999; 1-AUG-1999; 1-AUG-1999; 1-AUG-1999; 1-AUG-1999; 1-AUG-1999; 1-AUG-1999; 1-AUG-1999; 1-AUG-1999; 1-AUG-1999;
20-AUG-1999 20-AUG-1999 20-AUG-1999 20-AUG-1999 20-AUG-1999 20-AUG-1999 20-AUG-1999 20-AUG-1999 20-SUG-1999 20-SUG	5-AUG-1999; 99US 6-AUG-1999; 99US 6-AUG-1999; 99US 6-AUG-1999; 99US 9-AUG-1999; 99US 9-AUG-1999; 99US 1-AUG-1999; 99US
20-AUG-1999 20-AUG-1999 20-AUG-1999 20-AUG-1999 20-AUG-1999 20-BUS-01 25-AUG-1999 20-BUS-01 26-AUG-1999 20-BUS-01 27-AUG-1999 20-BUS-01 27-AUG-1999 20-BUS-01 27-AUG-1999 20-BUS-01 27-AUG-1999 20-BUS-01 27-AUG-1999 20-BUS-01 27-AUG-1999 20-BUS-01 27-BUS-01 27-BUS-01 28-BP-1999 20-BUS-01 28-BP-1999 20-BUS-01 28-BP-1999 20-BUS-01 29-BBP-1999 20-BUS-01 20-BBP-1999 20-BUS-01 21-BBP-1999 20-BUS-01 21-BBP-1999 20-BBP-1999 20-BBP-	5-AUG-1999; 99US-014 5-AUG-1999; 99US-014 6-AUG-1999; 99US-014 6-AUG-1999; 99US-014 9-AUG-1999; 99US-014 9-AUG-1999; 99US-014 1-AUG-1999; 99US-014
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11-MAY-1999
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2; Mismatches
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4.6e+02;
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Matches 6
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AC ABB65
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DE Drosc
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XX
DE Drosc
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ABB62955
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XX ABB62
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XX CPEKE
XX The 1
CC Capab
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                                                                                                                                                                                                                                                                                                                                                                                            capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL3051), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
Drosophila; dev pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                  Sequence 249 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated nucleic acid
genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABB62955 standard;
                                                  Drosophila melanogaster polypeptide SEQ ID NO 22848.
                                                                                   26-MAR-2002
                                                                                                                   ABB65352;
                                                                                                                                                 ABB65352 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 15657; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; ABL07058.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-MAR-2001; 2001WO-US009231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster polypeptide SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-MAR-2002
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                                                                                                                                                                                                                                                                                                Similarity 7; Conserv
                                                                                                                                                                                                                                  AGIVLGGQLI 101
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                 developmental biology; cell signalling; insecticide;
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                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                 protein; 249
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70.0%;
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                                                                                                                                                                                                                                                                                                                    Score 38;
Pred. No.
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4.6e+02;
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                                                                                                                                                                                                                                                                                                    1;
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Drosophila melanogaster.

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Best Local
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N-PSDB;
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11-JUL-2000; 2000US-00614150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cid interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLI6176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57373-ABL901840-ABL16175) and the encoded proteins (ABB57373-ABL901840-ABL901840-ABL901840-ABL901840-ABL901840-ABL901840-ABL901840-ABL901840-ABL901840-ABL901840-ABL901840-ABL901840-ABL901840-ABL901840-ABL901840-ABL901840-ABL901840-ABL901840-ABL901840-ABL901840-ABL901840-ABL901840-ABL901840-ABL901840-ABL901840-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (PEKE ) PE CORP NY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   interactions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADN73077 standard; protein; 249 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     plant; transgenic; E2Fa/DPa transcription factor; growth regulator; animal feed product; thale cress; cell wall biosynthesis; nitrogen metabolism; carbon metabolism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thale
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-JUL-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADN73077;
                                                                                                                                                                                                                                                                                                                                 WO2004035798-A2
                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana.
                                                                                                                                                                                                                                                            29-APR-2004
                                                                                                        18-OCT-2002; 2002EP-00079408.
                                                                                                                                                                                      20-OCT-2003;
                                      (CROP-) CROPDESIGN NV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cress protein upregulated in E2Fa/Dpa expressing plants SeqID
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7; Conservative
                                                                                                                                                                                      2003WO-EP011658
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Pred. No. 4.6e+02;
2; Mismatches 1
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Search completed: December Job time: 9.05036 secs

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2004, 09:16:30

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Query Match
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Matches 6
                                                                                                                                                                                                                                                                           the altered plant characteristics are selected from increased yield or physiology, altered endoreduplication, biochemistry, signal or physiology, altered endoreduplication, biochemistry, signal or physiology, altered endoreduplication, biochemistry, signal or physiology, storage lipid mobilisation and/or altered photosynthesis, transduction, storage lipid mobilisation and/or altered photosynthesis, transduction, storage lipid mobilisation of collary plants. Accordingly, these each relative to the corresponding wild type plants. Accordingly, these sequences can also be useful as positive or negative selectable markers sequences can also be useful as positive or negative selectable markers aduring transformation of cells or tissues. The identified genes play a during transformation or cabon metabolism or they function as wall biosynthesis, nitrogen and/or carbon metabolism or they function as wall biosynthesis, nitrogen and/or carbon metabolism or they function as the Effajpe transcription factors. This polypeptide sequence is thale cress protein the Effajpe transcription factor, given in an exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Altering plant characteristics, useful for producing plants for enzyme pharmaceutical production comprises modifying in a plant, expression of one or more nucleic acids and/or modifying level or activity of one or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Inze
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention relates to a novel method for altering one or more plant characteristics. Specifically, it refers to identifying genes that are up characteristics. Specifically, it refers to identifying genes that are up compared to the compared in transgenic plants overexpressing the heterodimeric expanying a transcription factor of Arabidopsis and using these sequences to Right plant characteristics accordingly. The present invention describes alter plant characteristics accordingly. The product invention of growth regulators, generating transgenic plants for the production of growth regulators, where enzymes, therapeutics, pharmaceuticals and animal feed products, where the product of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; ADN73076.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 972; 134pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                more proteins.
                                                                                                                                                            Sequence 249 AA;
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l Similarity
6; Conserv
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             Conservative
                                                     56.7%;
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                      Score 38; DB 8;
Pred. No. 4.6e+02;
2; Mismatches 1
                                                                                                           Length 249
                                   Indels
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scoring table:
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seq length: 2000000000
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67
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1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
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                      /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
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_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
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PUBCOMB.pep: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match	Match Length DB		ID	Description
_	45	67.2	123	17	US-10-425-115-267639	Sequence 267639
N	41	61.2	97	15	US-10-424-599-197757	Sequence
w	41	61.2	291	15	US-10-041-018-27	Sequence
4	41	61.2	319	14	US-10-156-761-9015	Sequence
տ	40	59.7	875	16	US-10-408-765A-1566	Seguenc
σ	39	58.2	178	15	US-10-335-977-5090	Sequence 5090, Ap
7	39	58.2	220	9	US-09-881-752A-16	Sequence 16, Appl
80	39	58.2	220	15	US-10-335-977-5091	Sequence 5091, Ap
9	39	58.2	403	15	US-10-425-114-48433	Sequenc
10	9	58.2	405	15	US-10-425-114-41675	Sequence
11	39	58.2	405	15	US-10-425-114-48462	Sequence
12	39	58.2	405	15	US-10-425-114-49554	Sequence
13	ود	58.2	419	21	US-10-282-122A-50158	Sequence 50158

45	44	43	42	41	40	96	38	37	36	35	34	u u	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14
38	38	38	38	38	38	38	38	38	38	38	38	38	38	38	38	38	38	38	38	38	38	38	38	38	39	39	39	39	39	39	39
σ.		ð	ð	0	ð	S)	σ	56.7	σ	σ	σ	σ	σ	σ	σ	σ	σ	σ	σ	σ	σ	σ	σ	σ	œ	8	8	œ	8	8	8
327	287	276	272	270	259	257	256	249	249	249	249	249	249	249	249	249	249	241	238	182	146	102	94	94	811	810	770	748	545	528	450
16	17	16	17	15	15	16	15	17	17	17	17	17	17	17	17	16	15	15	16	17	14	17	17	15	14	14	14	14	14	14	14
-10-437-963-15436	5-115-2	-10-437-963-14082	-10-425-115-28315	-10-425-114-	-10-425-114-	US-10-437-963-174771	-10-424-	-739-930-793	-10-425-115-2	-10-425-115-2	-10-425-115-2	5-115-2	-10-425-115-28316	-10-425-115-2	-10-425-115-	-10-437-963-17477	-10-424-599-	US-10-425-114-46558	-10-437-963-203	-10-425-115-227	-10-369-493-	-10-425-115-2	-10-425-115-3	-10-424-599-23165	-10-128-714-3	-10-128-714-823	-369-493-221	US-10-369-493-3245	-10-156-761-114	-10-369-493-217	US-10-402-842-30
Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	ø	æ	æ	æ	O	O	æ	Sequence	Sequence	Sequence	Sequence	æ	æ	ø	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
154362,	207790,	140821,	283158,	60462, A	41579, A	174771,		7930, Ap	284033,	283173,	283167,	283165,	283162,	231963,	231962,	174772,	205502,	46558, A	203753,	227826,	2228, Ap	294011,	365962,	1.1	•	N	,89	3245, Ap	11459, A	791,	0, Ar

ALIGNMENTS

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RESULT 1
US-10-425-115-267639
; Sequence 267639, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
RESULT 2
US-10-424-599-197757
; Sequence 197757, Application US/10424599
; Publication No. US20040031072A1
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; OTHER INFORMATION: Clone ID: MRT4577_175692C.1.pep
US-10-425-115-267639
                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 267639
LENGTH: 123
TYPE: PRT
                                                                                                                                                                                                                 Query Match 67.2%;
Best Local Similarity 63.6%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT FILLING DATE: 2003-04-28
CURRENT FILLING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Zea mays
                                                                                                                                    36
                                                                                                                               1 EFGAGLVLGGQ 11
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36 DYGSGLVIGGQ 46
                                                                                                                                                                                                                     4; Mismatches
                                                                                                                                                                                                                                         Score 45; DB
Pred. No. 14;
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                                                                                                                                                                                                                     Gaps
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PRIOR APPLICATION NUMBER: US 60/259880
PRIOR FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 413
SOPTWARE: PatentIn version 3.1
LENGTH: 291
TYPE: PRT
ORGANISM: Chlamydia trachomatis
US-10-041-018-27
                                                   GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROS
APPLICANT: SHIBA, TADAYOSH
APPLICANT: SAKAKI, YOSHIYU
APPLICANT: HATTORI, MASAHI
                                                                                                                                                                                                                               US-10-156-761-9015
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CURRENT APPLICATION NUMBER: US/10/424,599
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 197757
TYPE: ppr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 3
US-10-041-018-27
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                                                                                                                                                                                       Sequence 9015, Application US/10156761 Publication No. US20030119018A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Clone ID: PAT_MRT3847_205C.1.pep
US-10-424-599-197757
                         APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIHA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 27, Application US/10041018 Publication No. US20040072323A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Matsuda, Seiichi P.T.
APPLICANT: Hart, Elizabeth A.
TITLE OF INVENTION: Diterpene-Producing Unicellular Organism
FILE REFERENCE: P02080US1/10025547
CURRENT APPLICATION NUMBER: US/10/041,018
CURRENT APPLICATION NUMBER: 2002-01-07
POTCO APPLICATION NUMBER: 2002-01-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                              Local Similarity 63.6%; es 7; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity hes 8; Conserv
                                                                                                                                                                                                                                                                                            153 FGVGGILGGQY 163
APPLICATION NUMBER: US/10/156,761
                                                                                                                                                                                                                                                                                                                             2 FGAGLVLGGOF 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61.2%; Score 41; 72.7%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                       Score 41; DB 15; Length 291; Pred. No. 1.5e+02;
                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 15; Length 97;
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                                                                                                                                                                                                                                                                                                                                                        0;
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RESULT 6
US-10-335-977-5090
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                                                                                                                                                              Sequence 5090, Application US/10335977

Sequence 5090, Application US/10335977

Publication No. US20040052799A1

GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH et al
APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
RELATING TO HELICOBACTER PYLORI FOR
DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Homo sapiens US-10-408-765A-1566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:

APPLICANT: Ghosh, Soumitra S.
APPLICANT: Fahy, Edin D.

APPLICANT: Zhang, Bing
APPLICANT: Gibson, Bradford W.
APPLICANT: Taylor, Steven W.
APPLICANT: Glenn, Gary M.
APPLICANT: Glenn, Gary M.
APPLICANT: Warnock, Dale B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF ERG ID NOS: 15109
SEQ ID NO 9015
LENGTH: 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; SEQ ID NO 1566; LENGTH: 875; TYPE: PRT
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Best Local Similarity
Matches 8; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-408-765A-1566
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT ; ORGANISM: Streptomyces avermitilis US-10-156-761-9015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
59.7%; Score 40; DB 16; Length 875;
Best Local Similarity 54.5%; Pred. No. 6.5e+02;
Matches 6; Conservative 4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: WATHOCK, Dale B.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REFERENCE: 660088.465
CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1566, 1
Publication No.
ZIP: 02109-1875
COMPUTER READABLE FORM:
                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
                                                                                                                                                                                                                                                                                                                                                                                                          169 DESAGLIIGGK 179
                                                                                                                                                                                                                                                                                                                                                                                                                                             1 EFGAGLVLGGQ 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1566, Application US/10408765A
ion No. US20040101874A1
                                                      STREET: 28 State Str
CITY: Boston
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 GAGLYLGGQ 11
                                       COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                             28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61.2%;
                                                                                                                                                            10031
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APPLICANT: Kleanthous, Harold
APPLICANT: Kleanthous, Amal
APPLICANT: Miller, Charles
APPLICANT: Miller, Charles
APPLICANT: Oomen, Raymond P.
TITLE OF INVENTION: Identification of Polynucleotides
TITLE OF INVENTION: Genome
FILE APPLICATION: Genome
FILE APPLICATION NUMBER: US/09/881,752A
CURRENT APPLICATION NUMBER: US/09/881,752A
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 08/833,457
PRIOR REPERICES: 1997-04-01
SOFTWARE: F8stSEQ for Windows Version 4.0
SEQ ID NO 16
SEQ ID NO 5EQ ID NOS: 370
SEQ ID NO 179E: PRT
ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-881-752A-16
; Sequence 16, Application US/09881752A
; Patent No. US20020115078A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...178
SEQUENCE DESCRIPTION: SEQ ID NO: 5090:
US-10-335-977-5090
                                                                                                                                              US-09-881-752A-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                               Matches
                                                                               Query Match 58.2%;
Best Local Similarity 63.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 5090:
SEQUENCE CHARACTERISTICS:
LENGTH: 178 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 63.6%;
108 7; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/993,002
FILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTN-018
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows NT 4.0
SOFTWARE: UNIX
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORIGINAL SOURCE:
ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28
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3 GAGLVLGGQFM 13
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GFGVVLGGKFV 38
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COMPUTER: IBM PC Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 39; DB 15; Length 178; Pred. No. 1.8e+02;
                                                            Score 39; DB 9;
Pred. No. 2.3e+02;
3; Mismatches 1
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                                                               1; Indels
                                                                                                  Length 220;
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      APPLICANT
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NAME/KEY: misc feature;
LOCATION: (B) LOCATION 1...220;
SEQUENCE DESCRIPTION: SEQ ID NO: 5091:
US-10-335-977-5091
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                                                                                                                                               US-10-425-114-48433
Sequence 48433, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
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US-10-335-977-5091
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Publication No. US20040052799A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH et al
APPLICANT: DOUGLAS SMITH ET APPLICATION
DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                        APPLICANT: Liu, Jingdong APPLICANT: Zhou, Yihua
                                       APPLICANT:
                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 5091: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/993,002
FILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein HYPOTHETICAL: YES ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: GTN-018
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)27-7400
TELEFAX: (617)742-4214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: UNIX CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 10031
                                                                                                                                                                                                                                                                                                        70 GEGVVLGGKEV 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70 GFGVVLGGKFV 80
                                                                                                                                                                                                                                                                                                                             3 GAGLVLGGQFM 13
| |:||||:|:
Zhou, Yinua
Kovalic, David K
Screen, Steven F
: Tabaska, Jack E
: Cao, Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC Compatible OPERATING SYSTEM: Windows NT 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: LAHIVE & COCKFIELD STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 220 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                58.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                  Score 39; DB 15;
Pred. No. 2.3e+02;
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US-10-425-114-41675
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US-10-425-114-41675
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                                                                                                                                                                                    Sequence 48462, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
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Best Local S
Matches 7
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; OTHER INFORMATION: Clone ID: LIB3068-059-A10_FLI.pep
US-10-425-114-48433
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53131)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
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LENGTH: 405
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Publication No. US20040034888A1
GENERAL INFORMATION:
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TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
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Best Local 9
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LENGTH: 403
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APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, Dav
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ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53313) B CURRENT APPLICATION NUMBER: US/10/425,114 CURRENT FILING DATE: 2003-04-28 NUMBER OF SEQ ID NOS: 73128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Zea mays
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53.8%;
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53.8%;
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Pred. No. 4.3e+02;
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Pred. No.
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APPLICANT: Liu, Jingdong
APPLICANT: Xhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53313) B and Uses Thereof for Plant Improvement
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 49554
LENGTH: 405
TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                                                                              US-10-282-122A-50158; Sequence 50158; Application US/10282122A; Publication No. US20040029129A1; GENERAL INFORMATION:
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; OTHER INFORMATION: Clone ID: LIB3689-213-B12_FLI.pep
US-10-425-114-49554
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APPLICANT:
APPLICANT:
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FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
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Publication No. US20040034888A1
                                                                                                                                                                                                               APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carl
APPLICANT: Malone, Chery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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SEQ ID NO 48462
LENGTH: 405
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Best Local
                                                   TITLE OF INVENTION: Identification of Essential
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ORGANISM: Zea mays
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                                                                                 Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                 EFGAGLVLGGQFM 13
                                                                                                                                                                                   Haselbeck, Robert
Ohlsen, Kari
                                                                                                                                                      Wall,
                                                                                                                                                                    Zyskind, Judith
                                                                                                                                   Trawick, John
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53.8%;
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Pred. No. 4.3e+02;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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RESULT 15

US-10-369-493-21791

; Sequence 21791, Application US/10369493

; Publication No. US20030233675A1

; GENERAL INFORMATION:
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US-10-402-842-30
US-10-402-842-30
; Sequence 30, Application US/10402842
; Publication No. US20030219872A1
; GENERAL INFORMATION:
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Best Local Similarity
Matches 8; Conservi
                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Streptomyces hygroscopicus US-10-402-842-30
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US-10-282-122A-50158
                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Magarvey, Nathan A.
APPLICANT: Hucul, John A.
APPLICANT: Hucul, John A.
TITLE OF INVENTION: NON-RIBOSOMAL PEPTIDE SYNTHETASES AND ASSOCIATED BIOSYNTHETIC GEN
FILE REFERENCE: 0630/1J854-US1
CURRENT APPLICATION NUMBER: US/10/402,842
CURRENT FILING DATE: 2003-03-28
PRIOR APPLICATION NUMBER: US 60/368,713
PRIOR FILING DATE: 2002-03-30
SPRIOR FILING DATE: 2002-03-30
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin version 3.1
SEQ ID NO 30
LENGTH: 450
TYPE: PRT
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NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 50158
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PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
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PRIOR
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PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 2000-09-06
APPLICATION NUMBER: 60/230,347
FILING DATE: 2000-09-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/257,931 FILING DATE: 2000-12-22
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72.7%;
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                                                                                                                                                                                                                                Score 39; DB 14; Length 450; Pred. No. 4.8e+02; Indels 1; Mismatches 2; Indels
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Pred. No. 4.4e+02;
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US-10-369-493-3245
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APPLICANT: BAKAKI, YOSHIYUKI
APPLICANT: HATTORI, WASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: UP 2001-204089
PRIOR APPLICATION NUMBER: UP 2001-272697
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-08-02
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US-10-156-761-11459
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                     RESULT 17
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PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 21791
LENGTH: 528
TYPE: PRT
                                                                                                                                                                                                                                                                       SEQ ID NO 11459
LENGTH: 545
TYPE: PRT
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                                                                                                                                                                       Query Match
Best Local
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APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: OMURA, SATOSHI APPLICANT: IKEDA, HARUO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 15109
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                                                                                                                                                     Local Similarity 70.0
                                                                           332 AGLILGGLFL 341
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                                                                                                     4 AGLVLGGQFM 13
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                                                                                                                                                                       58.2%;
70.0%;
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                                                                                                                                                                       Score 39;
Pred. No.
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5.6e+02;
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Sequence 3245, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:

APPLICANT: Cao, APPLICANT: Hink APPLICANT: Slate

Hinkle, Gregory J. Slater, Steven C. Goldman, Barry S.

Yongwei

APPLICANT:

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RESULT 19
US-10-128-714-8235
; Sequence 8235, Application US/10128714
; Publication No. US20030119013A1
; GENERAL INFORMATION:
   APPLICANT: Jiang, Bo
; APPLICANT: Hu, Wengi
   APPLICANT: Tishkoff, Daniel
; APPLICANT: Zamudio, Carlos
; APPLICANT: Zamudio, Carlos
; APPLICANT: Eroshkin, Alexey M
; APPLICANT: Lemieux, Sebastien M
; APPLICANT: Lemieux, Sebastien M
; APPLICANT: Idenieux, Sebastien M
; APPLICANT: Idenieux, Sebastien M
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NAME/KEY: unsure
LOCATION: (1)..(748)
OTHER INFORMATION: unsure at all Xaa locations
US-10-369-493-3245
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US-10-369-493-22168
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PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 3245
LENGTH: 748
TYPR. DOT
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Best Local S
Matches 7
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US(10/369,493)
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 22168
LENGTH: 770
TYDE. DBT
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Best Local Similarity
Matches 7; Conserv
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TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
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ORGANISM: Neurospora crassa
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70.0%;
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Pred. No.
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Pred. No. 8e+02;
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APPLICANT: Jiang, Bo
APPLICANT: Hu, Wenqi
APPLICANT: Tishkoff, Daniel
APPLICANT: Zamudio, Carlos
APPLICANT: Zamudio, Carlos
APPLICANT: Zamudio, Carlos
APPLICANT: Zamudio, Carlos
APPLICANT: Lemieux, Sebastien M
APPLICANT: Longacole, Sepsition of Essential Genes in Aspergillus fumigatus and
ITILE OF INVENTION: Methods of Use
FILE REFERENCE: 10182-018-99
FILE REFERENCE: 10182-018-99
FILE REFERENCE: 10182-018-01
CURRENT APPLICATION NUMBER: US/10/128,714
CURRENT APPLICATION NUMBER: US/0/285,697
PRIOR FILING DATE: 2001-04-23
PRIOR FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: US/0/295,890
PRIOR APPLICATION NUMBER: US/0/295,890
PRIOR APPLICATION NUMBER: US/0/30,899
PRIOR APPLICATION NUMBER: US/0/316,362
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CURRENT APPLICATION NUMBER: US/10/128,714
CURRENT FILING DATE: 2002-04-23
CRICA REPLICATION NUMBER: US 60/285,697
PRIOR FILING DATE: 2001-04-23
PRIOR FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR FILING DATE: 2001-06-05
PRIOR FILING DATE: 2001-06-05
PRIOR FILING DATE: 2001-08-05
PRIOR FILING DATE: 2001-09-31
PRIOR APPLICATION NUMBER: US 60/316,362
PRIOR FILING DATE: 2001-09-31
NUMBER OF SEQ ID NOS: 8603
SOFTWARE: PATENTING PATENTING FURITHER TO SERVICE SER
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US-10-128-714-3235
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                                                                                                                                                                                                                                                                                                          ; ORGANISM: Aspergillus fumigatus US-10-128-714-3235
                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 3235
LENGTH: 811
TYPE: PRT
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn version 3.1
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    148 FSAGLVIGGK 157
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7; Conserva
                                                                             FGAGLVLGGQ 11
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70.0%;
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70.0%;
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Pred. No.
                                                                                                                                                               2; Mismatches
                                                                                                                                                                                                        Score 39; DB 14;
Pred. No. 8.7e+02;
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RESULT 23
US-10-425-115-294011
; Sequence 294011, Application US/10425115
; Publication No. US20040214272A1
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                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Clone ID: US-10-425-115-365962
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US-10-424-599-231652
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CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 365962
                                                                                                                                                                                               Query Match
Best Local Similarity
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SEQ ID NO 231652
LENGTH: 94
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Best Local Similarity
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APPLICANT: Kovalic David K
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5)22)18
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Kovalic, Dav. APPLICANT: Zhou, Yihua APPLICANT: Cao, Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: La Rosa, Thomas J. APPLICANT: Kovalic, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Nucleic Acid Molecules TITLE OF INVENTION: Plants
                                                                                                                                                                                                                                                                                                         LENGTH: 94
TYPE: PRT
ORGANISM: Zea mays
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NAME/KEY: unsure
LOCATION: (1)...194)
OTHER INFORMATION: unsure at all Xaa locations
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                                                                                                                                            3 GAGLVLGGQFM 13
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                                                                                                            GSHLILGGEFL
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                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plants
                                                                                                                                                                                                 56.7%;
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                                                                                                            79
                                                                                                                                                                                Score 38; DB
Pred. No. 1.4e
4; Mismatches
                                                                                                                                                                                                                                                                       MRT4577_96923C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PAT_MRT3847_51202C.1.pep
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Pred. No. 1.4e
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 15;
1.4e+02;
                                                                                                                                                                                                 1.4e+02;
                                                                                                                                                                                                                    DB 17; Length 94;
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US-10-425-115-227826, Application US/10425115; Sequence 227826, Application US/10425115; Publication No. US20040214272A1; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                              ; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(146)
; OTHER INFORMATION: unsure at all Xaa locations
US-10-369-493-2228
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US-10-369-493-2228
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                                                                     RESULT 25
                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 2228
LENGTH: 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2228, Application US/10369493 Publication No. US20030233675A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 294011
LENGTH: 102
                                                                                                                                                                                             Matches
                                                                                                                                                                                                             Query Match
Best Local
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: EXPRESSION OF MICROBIAL TITLE OF INVENTION: PLANTS WITH IMPROVED PRILE REFERENCE: 38-10(52052)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Kovalic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: La Rosa, Thomas
APPLICANT: ...Kovalic, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Zea mays
FEATURE:
                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Schizosaccharomyces pombe
                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity nes 7; Conserv
                                                                                                                       58 FGTGIILAGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93
                                                                                                                                                          2 FGAGLVLGGQ 11
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                                                                                                                           67
                                                                                                                                                                                                             56.7%;
                                                                                                                                                                                                             Score 38;
Pred. No.
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Pred. No.
                                                                                                                                                                                             Mismatches
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1.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AL PROTEINS PROPERTIES
                                                                                                                                                                                                                             DB 14;
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APPLICANT: La Rosa, Thomas J. APPLICANT: Kovalic, David K. APPLICANT: Zhou, Yihua

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; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_139373C.1.pep
US-10-425-115-227826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-437-963-203753; Sequence 203753, Application US/10437963; Publication No. US20040123343A1
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TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 227826
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US-10-437-963-203753
                                                                                                                                                                                                                              US-10-425-114-46558
                                                                                                                                                                                                                                                RESULT 27
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
APPLICANT: Li, Ping
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 203753
LENGTH: 238
LENGTH: 238
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                                                                                                                                                             Sequence 46558, Application US/10425114 Publication No. US20040034888A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                Matches
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TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                          APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94
                                                                                                                                                                                                                                                                                                               184
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7; Conserve
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70.0%;
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70.0%;
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Pred. No. 2.7e+02;
1; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                  Score 38; DB 16;
Pred. No. 3.6e+02;
1; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 238;
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OTHER INFORMATION: Clone ID: 700352025_FLI.pep US-10-425-114-46558
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LENGTH: 241
TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-424-599-205502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-424-599-205502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE SERENUCE: 38-21(5323)B
FILE SERENUCE: 38-21(5323)B
FURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 205502
LENGTH: 249
LENGTH: 249
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US-10-437-963-174772
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CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
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APPLICANT: Li Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules .
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules .
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement TILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 174772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                           GENERAL
                                                                                                                                                                                                                                                                                              Sequence 174772, Application US/10437963
Publication No. US20040123343A1
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                                                                                                                                                                                                                                       APPLICANT: La Rosa, Thomas
APPLICANT: Kovalic, David
                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Glycine max FEATURE:
                                                                                                                                                                                     APPLICANT:
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les 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                       132 FGCGVILGG 140
                                                                                                                                                                                                                                                                               INFORMATION:
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                                                                                                                                                                                                    Cao,
                                                                                                                                                                                                                       Kovalic, David
Zhou, Yihua
                                                                                                                                                 Boukharov, Andrey
Barbazuk, Brad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2;
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pred. No. 3.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and
TITLE OF INVENTION: Plants

FILE REFERENCE: 38-21(53222)B

CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 231962

LENGTH: 249

TYDE: DETERMINENT OF SERVICE AND SERVICE AND
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; OTHER INFORMATION: Clone ID:
US-10-437-963-174772
                                                                                                                                                                                                                                                                                                                                            APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322)B
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
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                                                                                                          ; OTHER INFORMATION: US-10-425-115-231963
                                                                                                                                                                                                                                                 SEQ ID NO 231963
LENGTH: 249
TYPE: PRT
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Best Local Similarity
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Zea mays
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                                                                                                                                       Clone ID:
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56.7%;
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                                                                                                                                   MRT4577_143143C.1.pep
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 38;
Pred. No.
Score 38; DB 17; Length 249; Pred. No. 3.8e+02;
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3.8e+02;
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US-10-425-115-283162
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US-10-425-115-283165
                                                                                                                                   ; OTHER INFORMATION: Clone ID: MRT4577_21344C.1.pep
US-10-425-115-283165
                                                                                                                                                                                                                                                                 APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules an
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322)B
FULB REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
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Best Local S
Matches 6
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CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 283162
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                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS:
SEQ ID NO 283165
LENGTH: 249
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Publication No. US20040214272A1
GENERAL INFORMATION:
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Best Local
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APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
                                                                                                                                                                TYPE: PRT
ORGANISM: Zea mays
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Clone ID: MRT4577_21341C.1.pep
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 249
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132 FGCGVILGG 140
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                                                                                  Score 38; DB 17;
Pred. No. 3.8e+02;
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                                                                                                 DB 17; Length 249;
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                                                                                                                                                                                                                                                                                                                                        and Other Molecules Associated With
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RESULT 34 US-10-425-115-283167

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APPLICANT: La ROSA, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Chou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules an
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322))B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 283173
LENGTH: 249
                                                           RESULT 36
US-10-425-115-284033
Sequence 284033, Application US/10425115
; Publication No. US20040214272A1
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; OTHER INFORMATION: Clone ID: MRT4577_21351C.1.pep
US-10-425-115-283173
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US-10-425-115-283173
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GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas
APPLICANT: Kovalic, David
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CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 283167
LENGTH: 249
TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                           Query Match
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Best Local Similarity 66.7%;
Matches 6; Conservative
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 388-21(5322)B
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NAME/KEY: unsure
LOCATION: (1)..(249)
OTHER INFORMATION: unsure at all Xaa locations
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                                                                                                                                                                                                                                                                   Local Similarity 66.
les 6; Conservative
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Pred. No.
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                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                       Length 249;
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; OTHER INFORMATION: Clone ID: ZEAMA-23APR03-C3166_22.p
US-10-739-930-7930
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US-10-424-599-205503
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Sequence 205503, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:
APPLICANT: Kosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Chou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 205503
LENGTH: 256
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: KOVALIC, DAVID K.

TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT FILE REFERENCE: 38-21(53377)B

CURRENT APPLICATION NUMBER: US/10/739,930

CURRENT FILING DATE: 2003-12-18

NUMBER OF SEQ ID NOS: 11088

SEQ ID NO 7930

LENGTH: 249
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Best Local 9
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LENGTH: 249
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APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322)18
CURRENT EPPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Zea mays
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ORGANISM: Zea mays
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 66.
                                                                                                                                                                                                                                                                                                                                                                                                 132 FGCGVILGG 140
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66.7%;
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Pred. No.
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Pred. No.
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ORGANISM: Glycine

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Query Match
Best Local Similarity
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Sequence 41579, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Li, Ping

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B

CURRENT APPLICATION NUMBER: US/10/437,963

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 174771
LENGTH- 257
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; OTHER INFORMATION: Clone ID: PAT_MRT3847_27598C.1.pep
US-10-424-599-205503
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APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 41579
LENGTH: 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 174771, Application US/10437963 Publication No. US20040123343A1 GENERAL INFORMATION:
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Best Local Similarity 66.7%;
Matches 6; Conservative
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yongwei
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NAME/KEY: unsure
LOCATION: (1)..(256)
OTHER INFORMATION: unsure at all Xaa locations
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Pred. No. 3.9e+02;
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Search completed: December Job time : 5.58273 secs
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                                                                                                                      Query Match 56.7%;
Best Local Similarity 66.7%;
Matches 6; Conservative
                                                                                                                                                                                                                    ORGANISM: Zea mays FEATURE:
                                                             142 FGCGVILGG 150
                                                                                          2 FGAGLVLGG 10
                                                                                                                                      Score 38; DB 15;
Pred. No. 3.9e+02;
                                                                                                                         Mismatches
                                                                                                                                                     DB 15; Length 259;
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Result
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Maximum DB
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                               Score
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Match
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           Published_Applications_AA:*
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/cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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/cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
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      US-09-313-942-8
US-09-935-868-8
US-10-287-035-8
4 US-10-287-035-8
4 US-09-313-942-15
US-09-313-942-15
US-10-287-035-15
4 US-10-287-035-15
4 US-10-322-696-144
US-09-313-942-26
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US-09-313-868-26
US-10-287-035-26
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Sequence 8, Appli
Sequence 8, Appli
Sequence 8, Appli
Sequence 12, Appli
Sequence 15, Appl
Sequence 15, Appl
Sequence 15, Appl
Sequence 15, Appl
Sequence 144, Appl
Sequence 26, Appl
Sequence 26, Appl
Sequence 26, Appl
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927	930	930.5	930.5	934	934	935	936.5	938.5	938.5	938.5	938.5	938.5	938.5	938.5	938.5	938.5	938.5	938.5	938.5	938.5	954.5	954.5	1683	1683	1683	1683	1783	1783	1783	1783	1788
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183	207	212	212	186	184	317	347	212	212	212	212	212	212	212	212	212	212	212	212	212	460	387	315	315	315	315	1168	1168	1168	1168	1158
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US-10-658-834A-198	US-10-264-049-3061	US-10-197-816-14	US-09-908-594-14	US-10-083-446-163	US-10-053-355A-3	US-10-083-446-145	US-10-763-619-8	US-10-276-642-6	US-10-866-540-13	US-10-828-343-3	US-10-773-654-13	US-10-774-149-13	US-10-773-939-13	US-10-440-464-61	US-10-298-148-13	US-10-400-708-13	US-10-400-377-13	US-10-099-007A-3	US-09-854-208-14	US-09-854-280-14		US-10-322-696-141	US-10-282-162-16	US-10-287-035-16	US-09-935-868-16	US-09-313-942-16	282-162-	035	US-09-935-868-24	2	US-10-282-162-26
Sequence 198, App	306	Sequence 14, Appl	14,	163	ω •	149	8	Sequence 6, Appli	13	Sequence 3, Appli	13,	13,	13,	61,	13,	13,	13	e 3, 1	Sequence 14, Appl	14,	Sequence 13, Appl	14	16	e 16,	16,	16,	24,	e 24	24, 1	24, 1	Sequence 26, Appl

ALIGNMENTS

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CURRENT APPLICATION NUMBER: US/09/313,942
CURRENT FILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: 09/313,942
PRIOR FILING DATE: 1999-05-19
PRIOR FILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: 60/101,858
PRIOR FILING DATE: 1999-09-25
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 8
SEQ ID NO 8
LENGTH: 592
TYPE: PAT
ORGANISM: Homo Bapiens
US-09-313-942-8
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US-09-313-942-8
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Publication No. US20020012962x1
GENERAL INFORMATION:
APPLICANT: REGENERON PHARMACEUTICALS, INC.
TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
TITLE OF INVENTION: AND USING
FILE REFERENCE: REG 203-A
                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 377; Conserv
121 CFRKSPLSNVVCEWGPRSTPSLTTKAVLLVRKFQNSPAEDFQEPCQYSQESQKFSCQLAV 180
                                                                                     61 VLRKPAAGSHPSRWAGMGRRLLLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPEEPQLS 120
                                                  61 VLRKPAAGSHPSRWAGMGRRLLLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPEEPQLS
                                                                                                                                                                               1 MLAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHW
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                                                                                                                                                                                                                                                  67.1%; Score 1921; DB 9; 77.1%; Pred. No. 3.7e-140; tive 22; Mismatches 44;
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APPLICANT: Regeneron Pharmaceuticals, Inc
TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making
FILE REFERENCE: REG 203D
FILE REFERENCE: REG 203D
CURRENT FILING DATE: 2002-04-11
CURRENT FILING DATE: 2002-04-11
PRIOR APPLICATION NUMBER: PCT/US99/22045
PRIOR FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 52
SOFTWARE: Patentin version 3.0
SEQ ID NO 8
DIENGTH: 592
TYPE: PRT
ORGANISM: Homo sapiens
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Best Local S
Matches 377
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US-10-28/-035-8

(Sequence 8, Application US/10287035)

Febblication No. US20030104567A1

Febblication No. US20030104567A1

FEBBLICANT: Neil Stahl and George D. Yancopoulos
APPLICANT: Neil Stahl and George D. Yancopoulos
TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, ANI
TITLE OF INVENTION: AND USING
FILE REFERENCE: REG 203DA

CURRENT FILING DATE: 2002-11-01
PRIOR APPLICATION NUMBER: USSN 09/935,868
PRIOR APPLICATION NUMBER: USSN 09/935,868
PRIOR APPLICATION NUMBER: USSN 09/787,835
PRIOR APPLICATION NUMBER: USSN 09/787,835
PRIOR APPLICATION NUMBER: USSN 09/313,942
PRIOR APPLICATION NUMBER: USSN 09/313,942
PRIOR APPLICATION NUMBER: 09/313,942
PRIOR APPLICATION NUMBER: 09/313,942
PRIOR APPLICATION NUMBER: 60/101,858
PRIOR APPLICATION NUMBER: 60/101,858
PRIOR FILING DATE: 1998-09-25
NUMBER OF SEG ID NOS: 60

SOPTWARE: FastSEQ for Windows Version 3.0

SECUENT: 592
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TYPE: PRT
ORGANISM: Homo sapiens
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Publication No. US20030143697A1

GENERAL INFORMATION:

APPLICANT: REGENERON PHARMACEUTICALS, INC.

APPLICANT: REGENERON PHARMACEUTICALS, INC.

APPLICATION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING TITLE OF INVENTION: AND USING

FILE REFERENCE: REG 203-B-US

CURRENT APPLICATION NUMBER: US/10/282,162

CURRENT FILING DATE: 2002-10-28

PRIOR FILING DATE: 1999-09-22

PRIOR PELING DATE: 1999-09-22

PRIOR FILING DATE: 1999-09-22

PRIOR FILING DATE: 1999-09-22
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 8
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22; Mismatches 44;
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RESULT 6
US-09-313-942-15
(Sequence 15, Application US/09313942
; Publication No. US20020012962A1
; Publication No. US20020012962A1
; GENERAL INFORMATION:
APPLICANT: REGENERON PHARMACEUTICALS, INC.
TITLE OF INVENTION: RECEPTOR BASED ANTAGONIS
TITLE OF INVENTION: AND USING
FILE REFERENCE: REG 203-A
; CURRENT APPLICATION NUMBER: US/09/313,942
; CURRENT FILING DATE: 1999-05-19
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APPLICANT: Gorman, Daniel M.
APPLICANT: Gorman, Daniel M.
APPLICANT: Bazan, J. Fernando
ITITLE OF INVENTION: Mammalian Receptor Proteins; Related Reagents and
ITITLE OF INVENTION: Methods
ITITLE OF INVENTION: Methods
ITILE REFERENCE: DX0992Q
CURRENT APPLICATION NUMBER: US/10/247,463
CURRENT FILING DATE: 2002-09-18
PRIOR APPLICATION NUMBER: US/09/588,113
PRIOR FILING DATE: 2000-05-31
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIN Ver. 2.0
1507WARE: PatentIN Ver. 2.0
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; TYPE: PRT
; ORGANISM: primate
US-10-247-463-12
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Best Local Similarity
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Pred. No. 4.6e-140;
                                                                                ANTAGONISTS, AND METHODS OF MAKING
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PRIOR FILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: 60/101,858
PRIOR FILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 15
                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Regeneron Pharmaceuticals, Inc
TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using
FILE REFERENCE: REG 203D
CURRENT APPLICATION NUMBER: US/09/935,868
CURRENT FILING DATE: 2002-04-11
PRIOR APPLICATION NUMBER: PCT/US99/22045
PRIOR FILING DATE: 1999-09-22
PRIOR FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 52
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SEQ ID NO 15
LENGTH: 360
TYPE: PRT
ORGANISM: Homo sapiens
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TYPE: PRT
ORGANISM: Homo sapiens
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Pred. No. 1.3e-139;
2; Mismatches 0;
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Pred. No. 1.3e-139;
2; Mismatches 0;
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CURRENT FILING DATE: 2002-11-01
PRIOR APPLICATION NUMBER: USSN 09/935,868
PRIOR FILING DATE: 2001-08-23
PRIOR PILING DATE: 2001-08-23
PRIOR PILING DATE: 2001-03-22
PRIOR PILING DATE: 105N 09/313,942
PRIOR FILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: USSN 09/313,942
PRIOR FILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: 09/313,942
PRIOR PILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: 60/101,858
PRIOR APPLICATION NUMBER: 60/101,858
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US-10-287-035-15
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Publication No. US20030104567A1
GENERAL INFORMATION:
APPLICANT: Neil Stahl and George D. Yancopoulos
TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS,
TITLE OF INVENTION: AND USING
FILE REFERENCE: REG 203DA
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SEQ ID NO 15
LENGTH: 360
TYPE: PRT
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NUMBER OF SEQ ID NOS: 60
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Local Similarity 99.4%;
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GEWSEWSPEAMGTPWTESRSPPAENEVSTPMQALTTNKDDDNILFRDSANATSLPVQ
                      GEWSEWSPEAMGTPWTESRSPPAENEVSTPMQALTTNKDDDNILFRDSANATSLPVE 357
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Pred. No. 1.3e-139;
2; Mismatches 0;
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APPLICANT: MOTTIS, David W.
APPLICANT: Malandro, Marc
TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
FILE REFERENCE: 529452001200
CURRENT APPLICATION NUMBER: US/10/322,696
CURRENT FILING DATE: 2003-10-17
NUMBER OF SEQ ID NOS: 186
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 144
LENGTH: 453
TYPE: PRT
                                                                                                                                                                                                                                                                     US-10-322-696-144
US-10-322-696-144
Sequence 144, Applicat
Publication No. US2006
GENERAL INFORMATION:
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CURRENT APPLICATION NUMBER: US/10/282,162
CURRENT FILING DATE: 2002-10-28
PRIOR APPLICATION NUMBER: 09/787,835
PRIOR FILING DATE: 1999-09-22
PRIOR APPLICATION NUMBER: PCT/US99/22045
PRIOR FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 56
SOPTWARE: FASESEQ for Windows Version 3.0
SEQ ID NO 15
LENGTH: 360
TYPE: PRT
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; ORGANISM: Homo sapiens
US-10-322-696-144
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Sequence 15, Application US/10282162
Publication No. US20030143697A1
GENERAL INFORMATION:
APPLICANT: REGENERON PHARMACEUTICALS, INC.
TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS,
TITLE OF INVENTION: AND USING
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Best Local Similarity
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o. US20040166490A1
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Pred. No. 1.3e-139;
2; Mismatches 0;
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Sequence 26, Application US/09313942

Publication No. US20020012962A1

GENERAL INFORMATION:

APPLICANT: REGENERON PHARMACEUTICALS, INC.

TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND USING

FILE REFERENCE: REG 203-A

CURRENT APPLICATION NUMBER: US/09/313,942

CURRENT FILING DATE: 1999-05-19

PRIOR APPLICATION NUMBER: 09/313,942

PRIOR FILING DATE: 1998-09-25

PRIOR APPLICATION NUMBER: 60/101,858

PRIOR APPLICATION NUMBER: 60/101,858

PRIOR APPLICATION NUMBER: 60/101,858

PRIOR FILING DATE: 1998-09-25

NUMBER OF SCT IN NCS. 12
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US-09-313-942-26
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 26
LENGTH: 1158
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Best Local Similarity
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181 PEGDSSFYIVSMCVASSVGSKFSKTQTFQGCGILQPDPPANITVTAVARNPRWLSVTWQD 240
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Pred. No. 2e-129;
2; Mismatches 1;
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RESULT 13
US-10-287-035-26
; Sequence 26, Application US/10287035
; Publication No. US20030104567A1
; Publication No. US20030104567A1
; GENERAL INFORMATION:
APPLICANT: Neil Stahl and George D. Yancopoulos
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AN
TITLE OF INVENTION: AND USING
FILE REFERENCE: REG 203DA
; CURRENT APPLICATION NUMBER: US/10/287,035
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: USSN 09/935,868
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US-09-935-868-26
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APPLICANT: Regeneron Pharmaceuticals, Inc
APPLICANT: Regeneron Pharmaceuticals, Inc
TITLE OF INVENTION: Receptor Based Antagonists,
FILE REFERENCE: REG 201D
CURRENT APPLICATION NUMBER: US/09/935,868
CURRENT FILING DATE: 2002-04-11
PRIOR APPLICATION NUMBER: PCT/US99/22045
PRIOR FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 52
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LENGTH: 1158
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ORGANISM: Homo sapiens
-09-935-868-26
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99.1%;
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PRIOR FILING DATE: 2001-08-23
PRIOR APPLICATION NUMBER: USSN 09/787,835
PRIOR FILING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: USSN 09/313,942
PRIOR APPLICATION NUMBER: USSN 09/313,942
PRIOR APPLICATION NUMBER: 09/313,942
PRIOR APPLICATION NUMBER: 09/313,942
PRIOR APPLICATION NUMBER: 60/101,858
PRIOR APPLICATION NUMBER: 60/101,858
PRIOR FILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 60
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 26
LENGTH: 1158
TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity 99.1
Matches 331; Conservative
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                                                                  GEWSEWSPEAMGTPWTESRSPPAENEVSTPMELL 334
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99.1%;
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pred. No. 2e-129;
2; Mismatches 1;
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US-10-282-162-26
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CURRENT FILING DATE: 2002-10-28
PRIOR APPLICATION NUMBER: 09/787,835
PRIOR FILING DATE: 1999-09-22
PRIOR APPLICATION NUMBER: PCT/US99/22045
PRIOR FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 56
SOFTWARE: PastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                               Sequence 26, Application US/10282162
Publication No. US20030143697A1
GENERAL INFORMATION:
APPLICANT: REGENERON PHARMACEUTICALS, INC.
APPLICANT: REGENERON PHARMACEUTICALS, INC.
TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
TITLE OF INVENTION: AND USING
FILE REFERENCE: REG 203-B-US
  Best Local Similarity Matches 331; Conserv
                                                                                                                                                                                SEQ ID NO 26
                                          Query Match
                                                                                                            ORGANISM: Homo sapiens
                                                                                                                                        TYPE: PRT
                                                                                                                                                           LENGTH: 1158
62.5%;
nilarity 99.1%;
Conservative
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                         Score 1788; DB 14;
Pred. No. 2e-129;
         Mismatches
                                                   Length 1158;
           Indels
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           Gaps
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APPLICANT: REGENERON PHARMACEUTICALS, INC.
TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, ANI
TITLE OF INVENTION: AND USING
FILE REFERENCE: REG 203-A
CURRENT APPLICATION NUMBER: US/09/313,942
CURRENT FILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: 09/313,942
PRIOR APPLICATION NUMBER: 09/313,942
PRIOR FILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: 60/101,858
PRIOR FILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 24
LENGTH: 1168
TYPE: PRT
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Local Similarity 99.7%;
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GEWSEWSPEAMGTPWTESRSPPAENEVSTPM 331
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Pred. No. 4.9e-129;
1; Mismatches 0;
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US-10-287-035-24
                                                CURRENT APPLICATION NUMBER: US/10/287,035
CURRENT FILING DATE: 2002-11-01
PRIOR APPLICATION NUMBER: USXN 09/935,868
PRIOR FILING DATE: 2001-08-23
PRIOR APPLICATION NUMBER: USXN 09/787,835
PRIOR APPLICATION NUMBER: USXN 09/787,835
PRIOR APPLICATION NUMBER: USXN 09/313,942
PRIOR FILING DATE: 1999-05-19
PRIOR FILING DATE: 1999-05-19
PRIOR FILING DATE: 1999-05-19
PRIOR FILING DATE: 1999-05-19
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Patent No. US20020164690A1
GENERAL INFORMATION:
APPLICANT: Regeneron Pharmaceuticals, Inc
TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using
FILE REFERENCE: REG 203D
CURRENT APPLICATION NUMBER: US/09/935,868
CURRENT FILING DATE: 2002-04-11
DBYTOD ADDITION NUMBER: 2002-04-11
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Publication No. US20030104567A1
GENERAL INFORMATION:
APPLICANT: Neil Stahl and George D. Yancopoulos
TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS,
TITLE OF INVENTION: AND USING
FILE REFERENCE: REG 203DA
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 24
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Best Local Similarity
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TYPE: PRT
                  APPLICATION NUMBER: 09/313,942 FILING DATE: 1999-05-19
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Pred. No. 4.9e-129;
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GENERAL INFORMATION:

APPLICANT REGEBERON PHARMACEUTICALS, INC.

APPLICANT REGEBERON PHARMACEUTICALS, INC.

TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND USING PILE REFERENCE: REG 203-B-US CURRENT APPLICATION NUMBER: US/10/282,162 CURRENT APPLICATION NUMBER: 09/787,835 PRIOR APPLICATION NUMBER: 09/787,835 PRIOR APPLICATION NUMBER: 09/787,835 PRIOR APPLICATION NUMBER: 09/9-22 PRIOR APPLICATION NUMBER: PCT/US99/22045 PRIOR APPLICATION NUMBER: PCT/US99/22045 PRIOR APPLICATION NUMBER: PCT/US99/22045 PRIOR APPLICATION NUMBER: PCT/US99/22045 PRIOR FILING DATE: 1999-09-22 NUMBER OF SEQ ID NOS: 56 SOFTWARE: FRASTSEQ for Windows Version 3.0 SEQ ID NO 24 LENGTH: 1168
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US-10-282-162-24
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NUMBER OF SEO ID NOS: 60
SOFTWARE: FastSEO for Windows Version
SEO ID NO 24
LENGTH: 1168
THE TENGTH: 1168
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ORGANISM: Homo sapiens
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                                                                                             Query Match
Best Local Similarity
Matches 330; Conserv
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ORGANISM: Homo sapiens
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  Conservative
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Pred. No. 4.9e-129;
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                                                                                                  Score 1783; DB 14;
Pred. No. 4.9e-129;
1; Mismatches 0;
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Sequence 16, Application US/09313942
publication No. US20020012962A1
publication No. US20020012962A1

GENERAL INFORMATION:
APPLICANT: REGENERON PHARMACEUTICALS, INC.
APPLICANT: REGENERON PHARMACEUTICALS, INC.
TITLE OP INVENTION: AND USING
FILE REFERENCE: REG 203-A
CURRENT FILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: 09/313,942
PRIOR APPLICATION NUMBER: 09/313,942
PRIOR FILING DATE: 1999-05-19
PRIOR FILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PASTSEQ for Windows Version 3.0
SEO ID NO 16
LENGTH: 315
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ORGANISM: Homo sapiens
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                                            PHSWNSSFYRLRFELRYRAERSKTFTTWWVKDLQHHCVIHDAWSGLRHVVQLRAQEEFGQ
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 GEWSEWSPEAMGT
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Pred. No. 4.5e-122;
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ANTAGONISTS,
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RESULT 20 US-09-958-868-16 ; Sequence 16, Application US/09935868 ; Patent No. US20020164690A1

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NESULT 21

US-10-287-035-16

Sequence 16, Application US/10287035

Publication No. US20030104587A1

GENERAL INFORMATION:
APPLICANT: Neil Stahl and George D. Yancopoulos
ITITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND
CURRENT APPLICATION NUMBER: US/10/287,035

CURRENT APPLICATION NUMBER: US/10/287,035

CURRENT FILING DATE: 2001-01-01

PRIOR APPLICATION NUMBER: USSN 09/315,868

PRIOR FILING DATE: 2001-03-22

PRIOR APPLICATION NUMBER: USSN 09/313,942

PRIOR APPLICATION NUMBER: USSN 09/313,942

PRIOR APPLICATION NUMBER: USSN 09/313,942

PRIOR RILING DATE: 1999-05-19

PRIOR APPLICATION NUMBER: 05/313,942

PRIOR FILING DATE: 1999-05-19

PRIOR APPLICATION NUMBER: 05/313,942

PRIOR FILING DATE: 1999-05-19

PRIOR APPLICATION NUMBER: 05/313,942

PRIOR FILING DATE: 1998-09-25

NUMBER OF SEQ ID NOS: 60

SOFTWARE: FASESEQ for Windows Version 3.0

1 LENGTH: 315
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APPLICANT: Regeneron Pharmaceuticals, Inc.

TITLE OF INVENTION: Receptor Based Antagonists, and

FILE REFERENCE: REG 203D

CURRENT APPLICATION NUMBER: US/09/935,868

CURRENT FILING DATE: 2002-04-11

PRIOR APPLICATION NUMBER: PCT/US99/22045

PRIOR FILING DATE: 1999-09-22

NUMBER OF SEQ ID NOS: 52

NUMBER OF SEQ ID NOS: 52

SOFTWARE: Patentin version 3.0

SEQ ID NO 16

LENGTH: 315

TYPE: PRT

ORGANISM: Homo sapiens
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; LENGTH: 315
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-287-035-16
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Pred. No. 4.5e-122;
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Sequence 16, Application US/10282162
Publication No. US20030143697A1
GENERAL INFORMATION:
APPLICANT: REGENERON PHARMACEUTICALS, INC.
TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF INTERFERENCE: REG 203-B-US
FILE REFERENCE: REG 203-B-US
CURRENT APPLICATION NUMBER: US/10/282,162
CURRENT FILING DATE: 2002-10-28
PRIOR APPLICATION NUMBER: US/10/282,162
CURRENT FILING DATE: 1999-09-22
PRIOR FILING DATE: 1999-09-22
PRIOR FILING DATE: 1999-09-22
PRIOR FILING DATE: 1999-09-22
PRIOR FILING DATE: 1999-09-22
SOPTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 16
TENCATURE: 1995-09-22
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Best Local Similarity 99.7
Matches 312; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                   LENGTH: 315
TYPE: PRT
ORGANISM: Homo
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                                                                    CFRKSPLSNVVCEWGPRSTPSLTTKAVLLVRKFQNSPAEDFQEPCQYSQESQKFSCQLAV 180
                                                                                                                               VLRKPAAGSHPSRWAGMGRRLLLLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPEEPQLS
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                                                                                                              VLRKPAAGSHPSRWAGMGRRLLLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPEEPQLS
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PEGDSSFYIVSMCVASSVGSKFSKTQTFQGCGILQPDPPANITVTAVARNPRWLSVTWQD
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Pred. No. 4.5e-122;
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                                                                                                                                                                                                                            Score 1683; DB 14;
Pred. No. 4.5e-122;
1. Mismatches 0;
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APPLICANT: MORTIS, DAVID W.
APPLICANT: MAIANDRO, MARC
TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
FILE REFERENCE: 529452001200
CURRENT APPLICATION NUMBER: US/10/322,696
CURRENT FILING DATE: 2003-10-17
NUMBER OF SEQ ID NOS: 186
SOFTWARE: FRSESEQ for Windows Version 4.0
SEQ ID NO 141
LENGTH: 387
TYPE: PRT
ORGANISM: Mus musculus
US-10-322-696-141
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US-10-322-696-141
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Publication No. US20040166490A1
GENERAL INFORMATION:
                                                                                                                                                       RESULT 24
US-10-247-463-13
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Best Local Similarity
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                                                                                                     Sequence 13, Application US/10247463
Publication No. US20030082734A1
GENERAL INFORMATION:
APPLICANT: Dowling, Lynette M.
APPLICANT: Timans, Jacqueline C.
APPLICANT: Gorman, Daniel M.
APPLICANT: Kastelein, Robert A.
APPLICANT: Bazan, J. Fernando
APPLICANT: Bazan, J. Fernando
TITLE OF INVENTION: Mammalian Receptor Proteins, Related Reagents and
TITLE OF INVENTION: Methods
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                                                                                                                                                                                                                                                                                                               QGEWSEWSPEAMGTPW-TESRSPPAENEVSTPMQALITINKDDDNILERDSANATSLPVEF 358
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                                                                                                                                                                                                                                                    MPVPPGEDSKDVAAP 373
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              ; ORGANISM: Homo sapiens
US-09-854-280-14
                                            TYPE: PRT
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APPLICANT: WOOD, William I.

TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES

PILE REPERENCE: P1381R1C2

CURRENT APPLICATION NUMBER: US/09/854,280

CURRENT FILING DATE: 2001-05-10

PRIOR APPLICATION NUMBER: US 09/311,832

PRIOR FILING DATE: 1999-05-14

PRIOR PILING DATE: 1999-05-14

PRIOR PILING DATE: 1998-05-15

PRIOR PILING DATE: 1998-05-15

PRIOR PILING DATE: 1998-05-15

PRIOR APPLICATION NUMBER: US 60/113,621

PRIOR PRIOR DATE: 1998-12-23

NUMBER OF SEQ ID NOS: 26
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LENGTH: 460
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/10/247,463
CURRENT FILING DATE: 2002-09-18
PRIOR APPLICATION NUMBER: US/09/588,113
PRIOR FILING DATE: 2000-05-31
NUMBER OF SEQ ID NOS: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 14, Application US/09854280 Patent No. US20020052027A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Chen, Jian
APPLICANT: Filvaroff,
APPLICANT: Goddard, I
APPLICANT: Gurney, A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            188; Conservative
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Gurney, Austin
Li, Hanzhong
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APPLICANT: Filvaroff, Ellen
APPLICANT: Filvaroff, Ellen
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Austin
APPLICANT: Usi, Hanzhong
APPLICANT: Wood, William I.
TITLE OF INVENTION: IL-17 HONOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: P1381-R1
CURRENT APPLICATION NUMBER: US/09/854,208
CURRENT FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: US/99/311,832
PRIOR APPLICATION NUMBER: US/99/311,832
PRIOR FILING DATE: 1998-05-14
PRIOR APPLICATION NUMBER: US 60/085,579
PRIOR FILING DATE: 1998-05-14
PRIOR FILING DATE: 1998-05-15
PRIOR FILING DATE: 1998-05-15
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US-09-854-208-14
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Best Local Similarity
Matches 187; Conserv
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SEQ ID NO 14
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Best Local Similarity
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TYPE: PRT
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                                                                                                                                            KEALAENNI.NI.PKWAEKDGCFQSGFNEETCI.VK.IITGILEFEVYLEYLQNRFESSEEQAR
                                                                                             AVQMSTKVLIQFLQKKAKNLDAITTPDPTTNASLLTKLQAQNQWLQDMTTHLILRSFKEF
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LOSSLRALROM 212
                                 LQSSLRALRQM 543
                                                                      AVOMSTKVLIQFLQKKAKNLDAITTPDPTTNASLLTKLQAQNQWLQDMTTHLILRSFKEF
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Pred. No. 1.5e-64;
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Pred. No. 1.5e-64;
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RESULT 27

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APPLICANT: COX III, George N

APPLICANT: COX III, George N

APPLICANT: Bolder Biotechnology, Inc.

FILE REFERENCE: 4152-1-PUS

CURRENT APPLICATION NUMBER: US/10/400,377

CURRENT FILING DATE: 2003-03-26

PRIOR APPLICATION NUMBER: US/09/462,941

PRIOR FILING DATE: 2000-01-14

PRIOR FILING DATE: 2000-01-14

PRIOR FILING DATE: 1997-07-14

NUMBER OF SEQ ID NOS: 41

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 13

LENGTH: 212

TYPE: PRT

ORGANISM: Homo Bapiens
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Publication No. US20030017150A1

GENERAL INFORMATION:
APPLICANT: Theodore Torphy
TITLE OF INVENTION: DERIVED PROTEINS, COMPOSITIONS, METHODS AND USES
FILE REFERENCE: CEN-0286
FILE REFERENCE: CEN-0286
CURRENT APPLICATION NUMBER: US/10/099,007A
CURRENT FILING DATE: 2002-03-14
NUMBER OF SEQ ID NOS: 17
SOOTWARB: Patentin Ver 2.0
SEQ ID NO 3
LENGTH: 212
TYDE: DET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 13, Application US/10400377 Publication No. US20030162949A1 GENERAL INFORMATION:
                                                                                                                                                              Query Match 32.8%;
Best Local Similarity 97.9%;
Matches 187; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 32.8%;
Local Similarity 97.9%;
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                   413 KEALAENNLNLPKMAEKDGCFQSGFNEETCLVKIITGLLEFEVYLEYLQNRFESSEEQAR
                                                                                                     354 LPVEF-MPVPPGEDSKDVAAPHRQPLTSSERIDKQIRYILDGISALRKETCNKSNMCESS
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KEALAENNLNLPKMAEKDGCFQSGFNEETCLVKIITGLLEFEVYLEYLQNRFESSEEQAR
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                                                                                                                                                              Score 938.5; DB 14; Length 212; Pred. No. 1.5e-64; 0; Mismatches 3; Indels 1;
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APPLICANT: COX III, George N
APPLICANT: Bolder Biotechnology, Inc.
APPLICANT: Bolder Biotechnology, Inc.
APPLICANT: Bolder Biotechnology, Inc.
TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
FILE REPERENCE: 4152-1-PUS
CURRENT APPLICATION NUMBER: US/10/400,708
CURRENT FILING DATE: 2003-03-26
CURRENT FILING DATE: 2003-03-26
PRIOR APPLICATION NUMBER: US/99/462,941
PRIOR APPLICATION NUMBER: US/99/462,941
PRIOR APPLICATION NUMBER: 60/052,516
PRIOR FILING DATE: 1997-07-14
NUMBER OF SEQ ID NUMBER: 60/052,516
PRIOR FILING DATE: 1997-07-14
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 13
LENGTH: 212
TYPE: PRI
ORGANISM: Homo sapiens
US-10-400-708-13
APPLICANT: Cox III, George N
APPLICANT: Bolder Biotechnology, Inc.
APPLICANT: APPLICATION NUMBER: US/10/298,148
CURRENT APPLICATION NUMBER: US/09/462,941
PRIOR APPLICATION NUMBER: US/09/462,941
PRIOR APPLICATION NUMBER: US/09/462,941
PRIOR APPLICATION NUMBER: 60/052,516
PRIOR APPLICATION NUMBER: 60/052,516
PRIOR APPLICATION NUMBER: 60/052,516
PRIOR FILING DATE: 1997-07-14
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 13
LENGTH: 212
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US-10-400-708-13
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Publication No. US20030171284A1
GENERAL INFORMATION:
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202 LOSSLRALROM 212
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APPLICANT: DEPRIMO, SAMUEL
APPLICANT: O'FARREIL, ANNE-MARIE
APPLICANT: MORIMOTO, ALYSSA
APPLICANT: SMOLICH, BEVERLY
APPLICANT: SMOLICH, BEVERLY
APPLICANT: MANNING, WILLIAM
APPLICANT: MALTER, SARAH
APPLICANT: CHERRINGTON, JULIE
APPLICANT: SCHILLING, JIM
APPLICANT: SCHILLING, JULIE
APPLICANT: SCHILLING, JULIE
APPLICANT: SCHILLING, JULIE
APPLICANT: SCHILLING, JULIE
APPLICANT: NOVEL BIOMARKERS OF TYROSINE KINASE INHIBITOR EXPOSURE
TITLE OF INVENTION: AND ACTIVITY IN MAMMALS
TITLE OF INVENTION: NUMBER: 60/380,872
PRIOR APPLICATION NUMBER: 60/380,872
PRIOR APPLICATION NUMBER: 60/448,922
PRIOR APPLICATION NUMBER: 60/448,922
PRIOR FILING DATE: 2003-02-24
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; ORGANISM: HOI
US-10-298-148-13
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US-10-440-464-61
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; Publication No. US200
; GENERAL INFORMATION:
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US-10-440-464-61
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LENGTH: 212
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413 KEALABNNLNLPKWAEKDGCFOSGFNEETCLVKIITGLLEFEVYLEYLQNRFESSEEQAR
                                                                               82 KEALAENNINLPKWAEKDĠĊFQSĠFNEETCLVKIITGLLEFEVYLEYLQNRFESSEEQAR
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Pred. No. 1.5e-64;
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Pred. No. 1.5e-64;
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APPLICANT: Cox III, George N
APPLICANT: Bolder Biotechnology, Inc.
FILE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
FILE REFERENCE: 4152-1-PUS
CURRENT APPLICATION NUMBER: US/10/774,149
CURRENT FILING DATE: 2004-02-05
PRIOR APPLICATION NUMBER: US/10/400,377
PRIOR APPLICATION NUMBER: US/09/462,941
PRIOR FILING DATE: 2003-03-26
PRIOR APPLICATION NUMBER: US/09/462,941
PRIOR APPLICATION NUMBER: US/09/462,941
PRIOR FILING DATE: 2000-01-14
PRIOR APPLICATION NUMBER: US/09/462,941
PRIOR FILING DATE: 1997-07-14
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 13
LENGTH: 212
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; SOFTWARE: PATENTIN VET. 2.0
; SEQ ID NO 13
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-773-939-13
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Sequence 13, Application US/10774149

Publication US20040175800A1
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US-10-773-939-13
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Matches 187; Conserv
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APPLICANT: Cox III, George N
APPLICANT: Bolder Biotechnology, Inc.
APPLICANT: Bolder Biotechnology, Inc.
TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
FILE REFERENCE: 4152-1-PUS
CURRENT APPLICATION NUMBER: US/10/773,939
CURRENT FILING DATE: 2004-02-05
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PRIOR FILING DATE: 2003-03-26
PRIOR APPLICATION NUMBER: US/09/462,941
PRIOR FILING DATE: 2000-01-14
PRIOR APPLICATION NUMBER: 60/052,516
PRIOR FILING DATE: 1997-07-14
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Conservative
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US-10-773-654-13
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Best Local Similarity 97.9
Matches 187; Conservative
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Best Local Similarity
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APPLICANT: Bolder Biotechnology, Inc.
APPLICANT: Bolder Biotechnology, Inc.
TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
FILE REFERENCE: 4152-1-PUS
CURRENT APPLICATION NUMBER: US/10/773,654
CURRENT FILING DATE: 2004-02-05
PRIOR APPLICATION NUMBER: US/10/400,377
PRIOR FILING DATE: 2003-03-26
PRIOR APPLICATION NUMBER: US/09/462,941
PRIOR APPLICATION NUMBER: US/09/462,941
PRIOR APPLICATION NUMBER: 60/052,516
PRIOR APPLICATION NUMBER: 60/052,516
PRIOR FILING DATE: 1997-07-14
NUMBER OF SEQ ID NOS: 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 212
                                                                            142
                                                                                                                 473
                                                                                                                                                                                                                                                              354 LPVEF-MPVPPGEDSKDVAAPHRQPLTSSERIDKQIRYILDGISALRKETCNKSNMCESS 412
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                                                                                                                                                                                413 KEALAENNLNLPKMAEKDGCFQSGFNEETCLVKIITGLLEFEVYLEYLQNRFESSEEQAR 472
  202
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                                                                                                       AVQMSTKVLIQFLQKKAKNIDAITTPDPTTNASLITKLQAQNQWLQDMTTHLIILRSFKEF 532
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                                     LOSSLRALROM 543
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                                                                            AVQMSTKVLIQFLQKKAKNLDAITTPDPTTNASLLTKLQAQNQWLQDMTTHLILRSFKEF
                                                                                                                                                         KEALAENNLNLPKMAEKDGCFQSGFNEETCLVKIITGLLEFEVYLEYLQNRFESSBEQAR
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LOSSLRALROM 212
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Pred. No. 1.5e-64;
0; Mismatches 3;
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Pred. No. 1.5e-64;
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RESULT 35 US-10-828-343-3 , Sequence 3, Application US/10828343

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Publication No. US20040228838A1
GENERAL INFORMATION:
APPLICANT: FLECKENSTEIN, Bernhard
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 RESULT 36
US-10-866-540-13
j. Sequence 13, Application US/10866540
j. Publication No. US20040230040A1
j. GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                  Matches 187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (202) 672-53V
TELEPAX: (202) 672-5399
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/10/828,343
FILING DATE: 21-Apr-2004
CLASSIFICATION UNMBER: US/09/230,048
APPLICATION NUMBER: US/09/230,048
PILING DATE: 12-Mar-1999
APPLICATION NUMBER: WO PCT/EP96/03199
PILING DATE: 19-UUL-196
ATTORNEY/AGENT INFORMATION
NAME: Granadon. Patricia D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: VIRAL INTERLEUKIN-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Granados, Patricia D.
REGISTRATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 058315/0129
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                      413
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CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 212 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                      KBALAENNINIPKMAEKOGCFOSGFNEETCLYKIITGILEFEVYLEYLQNREESSEEQAR 472
                                                                                                                                                                                                                                                    LOSSLRALROM 543
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nilarity 97.9%;
Conservative
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NEIPEL, Frank
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Pred. No. 1.5e-64;
                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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; TYPE: PRT ; ORGANISM: Homo sapiens US-10-866-540-13
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                                                                                                                                                                                                                                                                   APPLICANT: Ralph, Stephen John
TITLE OF INVENTION: IMMUNE POTENTIATING COMPOSITIONS
TITLE OF INVENTION: IMMUNE POTENTIATING COMPOSITIONS
FILE REFERENCE: DAVIZ200.001APC
CURRENT APPLICATION NUMBER: US/10/276,642
CURRENT FILING DATE: 2002-11-15
PRIOR APPLICATION NUMBER: PCT/AU01/00565
PRIOR PILING DATE: 2001-05-17
PRIOR PILING DATE: 2001-05-17
PRIOR PILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 20
SOPTWARE: FASTSEQ for Windows Version 4.0
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US-10-276-642-6
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 13
LENGTH: 212
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APPLICANT: Bolder Biotechnology, Inc.
APPLICANT: Bolder Biotechnology, Inc.
FILE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
FILE REFERENCE: 4152-1-PUS
CURRENT APPLICATION NUMBER: US/10/866,540
CURRENT FILING DATE: 2004-06-10
CURRENT FILING DATE: 2004-06-10
PRIOR FILING DATE: 2003-03-26
PRIOR FILING DATE: 2003-03-26
PRIOR APPLICATION NUMBER: US/09/462,941
PRIOR APPLICATION NUMBER: US/09/462,941
PRIOR PILING DATE: 2000-01-14
PRIOR PILING DATE: 2000-01-14
PRIOR FILING DATE: 1997-07-14
PRIOR FILING DATE: 1997-07-14
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                                                                                                                                                                                                                                          SEQ ID NO 6
LENGTH: 212
                                                                                                                        Matches
                                                                                                                     Best Local Similarity Matches 187; Conserv
                                                                                                                                                    Query Match
                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
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Local Similarity 97.9%;
es 187; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22 LPAAFPAÞVÞÞGEDSKDVÁÁÞHKÓÞLTSSERÍDKÓÍRÝÍLDGÍSÁLRKETCNKSNMCESS 61
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413 KBALAENNUNLPKWAEKDGCFOSGFNEETCLVKIITGLLEFEVYLEVLQNRPESSEEQAR 472
                                                     354 LPVEF-MPVPPGEDSKOVAAPHRQPLTSSERIDKQIRYILDGISALRKETCNKSNMCESS
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milarity 97.9%;
Conservative (
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Pred. No. 1.5e-64;
                                                                                                                                0;
                                                                                                                              Score 938.5; DB 17;
Pred. No. 1.5e-64;
0; Mismatches 3;
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Sequence 8, Application US/10763619
Publication No. US20040215008A1
GENERAL INFORMATION:
APPLICANT: Biochemie Gesellschaft m.b.H.
TITLE OF INVENTION: Production of proteins
FILE REFERENCE: G-31109/A/BCK
CURRENT APPLICATION NUMBER: US/10/763,619
CURRENT FILLING DATE: 2004-01-23
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                RESULT 39
US-10-083-446-145
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US-10-763-619-8
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                                                                                                                                                                                                                                                                         Sequence 145, Applicat Publication No. US2003 GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: Oligo-histidine purification aid combined with OTHER INFORMATION: sequences of Pestivirus and Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 347
TITLE OF INVENTION: Methods Of Ex-Vivo Expansion Of Hematopoietic Cells
Using Multivariant (IL-3) Hematopoiesis Chimera Proteins
NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                 331
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                                                                                                                                                                                                                                                                                                                                                                                                                 RSFKEFLQSSLRALROM 347
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b. US20030185790A1
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                                                                           Caparon, Maire H.
Easton, Alan M.
Klein, Barbara K.
McKearn, John P.
Olins, Peter O.
Paik, Kumnan
Thomas, John W.
                                                                                                                                                                                                            Abrams, Mark A.
Bauer, S. C.
Braford-Goldberg,
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Pred. No. 4.4e-64;
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RESULT 40
US-10-053-355A-3
; Sequence 3, Application US/10053355A
; Publication No. US20030077824A1
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APPLICATION UNMBER: 08/762,227

FILING DATE: 09-DEC-1996

APPLICATION NUMBER: US 08/192,325

FILING DATE: 14-FEB-1994

APPLICATION NUMBER: US 08/446,872

FILING DATE: 06-JUN-195

ATTORNEY/AGENT INFORMATION:

NAME: S. Christopher Bauer

REGISTRATION NUMBER: 42,305

REFERENCE/DOCKET NUMBER: C-2790/6

TELEPHONE: (636)737-6257

TELEPHONE: (636)737-6257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 145:
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CURRENT APPLICATION DATA:
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STATE: Missouri
COUNTRY: USA
                                                                                                                                       LQDMTTHLILRSFKEFLQSSLRALRQM 543
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DPNNLNSEDMDILMERNLRTPNLLAFVR-AVKHLENASGIEAILRNLQPCLPSATAAPSR
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FILING DATE: 26-Feb-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: S. Christopher Bauer, Pharmacia Corporation
Corporate Patent Dept., Mail Zone O4E
STREET: 800 N. Lindbergh
                                                                                                                     LODMITHLILRSFKEFLOSSLRALROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                      SGGGSNM----APVPPGEDSKDVAAPHROPLTSSERIDKQIRYILDGIS 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32.7%; Score 935; DB 1.63.0%; Pred. No. 5e-64;
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Search comp Job time :				Query Match Best Local Similarity Matches 184; Conser	GENERAL INFORMATION: APPLICANT: ROSSI, Alex TITLE OF INVENTION: Pr TITLE OF INVENTION: SI FILE REFERENCE: A-7088 FILE REFERENCE: A-7088 FILE REFERENCE: A-7088 FILE REFERENCE: A-7080 F
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leted: Decem 193.417 secs	543 184		ISD 	ity	Ale Ale 708 NUI NUI 200S
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Maximum Match 100%
Listing first 45 summaries
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Match
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2: uniprot_trembl:*
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67
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  GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Q8BRE3
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Q6FPT7
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Q9RS23
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Q7CVA1
NIFJ_K
                                                   Q8HG38
Q6L0E6
Q7ZSZ2
CYSH_S)
Q8KMM1
                                                                                                                                         Q82N27
Q6FMS6
Q916G8
Q74EW6
                                                                                                                        AAR34173
YFE9_YEAST
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Ass53165 ashbya go
Q9r823 deinococcus
Q6cc56 yarrowia li
Q92p15 rhizobium m
Q84633 chlamydia t
Q12067 saccharomyc
Ass56363 saccharomyc
Q82n27 streptomyce
Q6fms6 candida gla
Q9i6g8 pseudomonas
Q74ew6 geobacter s
Aar34173 geobacter
P43554 saccharomyc
Q6fpt7 candida gla
P96289 mycobacteri
Q7nje3 gloeobacteri
Q7nje3 gloeobacteri
Q8hmg38 alligator s
Q610e6 picrophilus
Q7zszz xenopus lae
Q5309 synechococc
Q8kmnl leuconostoc
Cad24411 leuconostoc
Cad24411 leuconostoc
Cad24411 tropheryma
Q8bre3 mus musculu
Q83h15 tropheryma
Q8bre3 mus musculu
Q93744 caulobacter
Q754e9 ashbya goss
                                                                                                                                                                                                                                       Q8u787 agrobacteri
Q7cval agrobacteri
P03833 klebsiella
Q755m3 ashbya goss
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}		SQ KW	RC RA	9 I A F F F B B 20000 X X F	교 교 대	
	Query Match Best Local Matches	Scien EMBL; PIR; PIR; Inter Inter Inter Pfam; Compl		U78	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	3
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Q 11 Q 235	68. Y 80. rvative	323 (2001). 145361.1; - 8; 8; 8; 8; Wing_hlx; 1; 1.	PubMed=1174 I J.C., Kaul Y., Chen L., I.T., Eisen Denning J., D R., Li MJ G., Saemphi Tao Y., Bid Jiao L., Kim By S.V., Tomb Per natural ge	TERMILE . TERMBLE . TERMBLE . TERMBLE . TERMBLE . Al regulato ames = Atu456 tume facien tume facien teobacteria Rhizobium/, 6299;	555 579 623 681 745 826 875 897 111 1617 111 129 200 220	n n n
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	Score 46; DB 2; Length Pred. No. 22; 1; Mismatches 1; Ind	lx_DNA_bnd. W; 77DF5D6C2F279C20 CRC64	13193; 1 R., Monks D.E., Kitajim J.A., Karp P.D., Bovee D J.A., Karp P.D., Bovee D J.A., Composition of the	TEMBLrel. 21, Created) TEMBLrel. 21, Last sequence update) TEMBLrel. 26, Last annotation update) TEMBLrel. 26, Last annotation update) I regulator, ROX family. Inmes=Atu4567; Itumefaciens (strain C58 / ATCC 33970). Tumefaciens (strain C58 / ATCC 34970). Temporation of the property of t	AASS 34 92 Q9KPJ7 Q7TMM1 Q8C751 Q8CFS2 Q8CVR6 Q9YX34 DD10 HUMAN Q8OY44 Q9SKV5 Q92MB6 Q7R2LB Q92MB6 Q9BDD4 Q92KA5 ALIGNMENTS	270
	382; els 0; Gaps		Jr., Woo L., Jr., Woo L., Sr., Grant C., gri A., Gordon D., o P., Gordon D., -Y., Dolan M., -Y., Dolan M., on M.V.,	iales; erium.		aghhva o
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RESULT 2
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ID Q7CVA1 PRELIMINARY;
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RESULT
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P0383; P09112;
21-7UL-1986 (Rel. 01, Created)
01-MAR-1989 (Rel. 10, Last sequence up
05-7UL-2004 (Rel. 44, Last annotation
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Matches 8
        SEQUENCE OF 1-127
MEDLINE=83246546;
Shen S., Xue Z., I
                                                                           MEDILINE-93247479; PubMed-8483412; Charlton W., Cannon W., Buck M.; The Klebsiella pneumoniae nifJ promoter: a activation by the NifA
                                                                                                                                                                                                            Cannon M.,
Beynon J.;
                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                          Arnold W., Rump A., Klipp W., Priefer U.B., Puehler A., "Nucleotide sequence of a 24,206-base-pair DNA fragment carryin entire nitrogen fixation gene cluster of Klebsiella pneumoniae. J. Mol. Biol. 203:715-738(1988).
                                                                                                                                                   REVISIONS,
                                                                                                                                                                                                                                           MEDLINE=89083580;
                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=89094839; PubMed=3062178;
                                                                                                                                                                                                                                                                                                                                                                                                Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Klebsiella.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-2108551; PubMed=11743194; Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Goodner B., Hinkle G., Gattung S., Miller N., Halling C., Mullin L., Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L., Houmtel K., Gordon J., Voudin M., Iartchouk O., Epp A., Liu F., Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B., Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G., Cielo C., Slater S.; "Genome sequence of the plant pathogen and biotechnology agent Agrobacterium tumefaciens C58."; Science 294:2323-2328 (2001).
                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=573;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Klebsiella pneumoniae.
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InterPro; IPR0096600; ROK.
InterPro; IPR009058; Wing_hlx_DNA_bnd.
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NCBI_TaxID=176299;
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OrderedLocusNames=AGR_L_609;
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AGR_L_609p.
                                                                                                                                                                      nucleotide sequence of the nifJ gene of sic Acids Res. 16:11379-11379(1998).
                                                                        Microbiol.
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                                                               regulating activation by the robiol. 7:1007-1021(1993).
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8; Conserv
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                                                                                                                            SEQUENCE FROM N.A.
247479; PubMed=8483412;
                                                                                                                                                                                                                           Cannon
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7 FROM N.A.
PubMed=6306580;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ROK;
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                                                                                                                                                                                                                                     PubMed=3060860;
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annotation updat
eductase (EC 1.2.
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Pred. No. 23;
1; Mismatches
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ACCOMPAND ACCOMP

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Q755M3;
05-JUL-2004 (TrEMBLrel. 2:
05-JUL-2004 (TrEMBLrel. 2:
05-JUL-2004 (TrEMBLrel. 2:
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Best Local
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EMBL; X13303; CAA31665.1; -.

EMBL; X13309; CAA31601.1; -.

PIR; S01997; QQKBFP.

HSSP; P94692; IKEK.

InterPro; IPR009151; Helical ferredoxin.

InterPro; IPR002869; POR N.

InterPro; IPR002880; POR N.

InterPro; IPR002890; Pyruvate decarb.

InterPro; IPR00399; Pyruvate decarb.

InterPro; IPR009014; Transketo_C_like.

Pfam; PP00137; Fer4; 2.

Pfam; PP001578; POR; 1.

Pfam; PP01558; POR; 1.

Pfam; PP01558; POR; 1.

Pfam; PP01579; TPP_enzyme_C; 1.

PROSITE; PS00199; 4FE45; FERREDOXIN; 2.

4Fe-45; Electron transport; Iron-sulfur;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "An Ope...
pneumoniae.",
pneumoniae.",
Nucleic Acids Res. 11:4241----
-I- FUNCTION: Oxidoreductase re
-rom pyruvate to flavodoxi
-rom pyruvate to flavodoxi
-rom pyruvate to flavodoxi
SEQUENCE FROM N.A. STRAIN=ATCC 10895; PubMed=15001715;
                                                                   Ashbya gossypii (Yeast) (Eremothecium gossypii).
Eukaryota; Fungi; Ascomycota; Saccharomycotina;
                                           Saccharomycetales;
NCBI_TaxID=33169;
[1]
                                                                                                    AFL209Wp.
Name=AFL209W;
                                                                                                                                                                                                                                                                                                                                                 METAL
CONFLICT
SEQUENCE
                                                                                                                                                                                                          4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMML outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way endified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                               873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   leic Acids Res. 11:4241-4250(1983).
FUNCTION: Oxidoreductase required for the transfer of ele from pyruvate to flavodoxin, which reduces nitrogenase.
CATALYTIC ACTIVITY: Pyruvate + CoA + oxidized flavodoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CoA + CO(2) + reduced
SIMILARITY: The iron-s
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72.7%;
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Pred. No. 60;
2; Mismatches
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Iron-sulfur 1 (4Fe-4S)
Iron-sulfur 1 (4Fe-4S)
Iron-sulfur 2 (4Fe-4S)
Iron-sulfur 2 (4Fe-4S)
Iron-sulfur 2 (4Fe-4S)
Iron-sulfur 2 (4Fe-4S)
                                                                   Saccharomycotina; Saccharomycetes;
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A -> R (in F
                                                                                                                        sequence update)
annotation updat
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Best Local S
Matches 8
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Q9RS23;
01-MAY-2000 (TrEMBLrel. 13, Cr
01-MAY-2000 (TrEMBLrel. 13, La
01-MAR-2004 (TrEMBLrel. 26, La
Hypothetical protein DR2304.
OrderedLocusNames=DR2304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The Ashbya gossypii genome as a tool Saccharomyces cerevisiae genome."; Science 304:304-307(2004).
EMBL; AE016899; TASS3165.1; -
SEQUENCE 160 AA; 17720 MW; 3852786
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AGD; /
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SEQUENCE FROM N.A.

STRAIN-R1 / ATCC 13939 / DSM 20539 / NCIB 9279;

MEDLINE=20036896; PubMed=10567266;

White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=15001715;
Dietrich F.S., Voegeli S., Brachat S., Lerch A., Gates K., S Mohr C., Poblmann R., Luedi P., Choi S., Wing R.A., Flavier Gaffney T.D., Philippen P.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ashbya gossypii (Yeast) (Eremothecium gossypii).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Eremothecium.
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                                                                                                                                                                                                         NCBI_TaxID=1299;
                                                                                                                                                                                                                                                                                         Bacteria;
                                                                                                                                                                                                                                                                                                                      Deinococcus radiodurans.
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Pred. No.
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01-OCT-2004
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01-OCT-2004 (TrEMBLrel. 28, Last sequence update)
01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Chromosome C of strain CLIB99 of Yarrowia lipolytica.
                                                                                                                                                                                                                                                                                                                                    Genoscope;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases
EMBL; CR382129; CAG82066.1; -.
SEQUENCE 540 AA; 58440 MW; BCC2AE9995C981AF CRC64;
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Yarrowia lipolytica (Candida lipolytica).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          radiodurans R1.";
Science 286:1571-1577(1999).
EMBL; AB002062; ARF11854.1;
PIR; B75290; B75290.
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396 AA; 39229 MW; 355FCB5E0179F312 CRC64;
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A Boistard P., Becker A., Boutry M., Cadieu E., Dreno S., Gloux S.,
A Godzie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
A Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U.,
A Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;
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Sinorhizobium meliloti strain 1021.";
Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
R EMBL, AL591789; CAC45561.1;
PROG. 05:0016021; C:integral to membrane; IEA.
Complete proteome; Hypothetical protein; Transmembrane.
SEQUENCE 155 AA; 17944 MW; 0A3B12286D1FDAFA CRC64;
                                                                                                                                                                                                                                                                               01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Gerany-Jerany-1 pyrophosphate synthase.
Name=ispA; OrderedLocusNames=CT628;
Chlamydia trachomatis.
Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae;
SEQUENCE FROM N.A.
STRAIN=D / UW-3 / Cx;
MEDLINE=99000809; PubMed=9784136;
Stephens R.S., Kalman S., Lammel C.
Mitchell W.P., Olinger L., Tatusov
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Galibert F., Finan T.M., Long S.R., Buehler A., Abola P., Ampe F.,

Barloy-Hubler F., Barnett M.J., Becker A., Boistard P., Bothe G.,

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Cowie A., Davis R.W., Dreano S., Federspiel N.A., Fisher R.F.,

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Hernandez-Lucas I., Hong A., Huizar L., Hyman R.W., Jones T., Kahn D.,

Kahn M.L., Kalman S., Keating D.H., Kiss E., Komp C., Lelaure V.,

Masuy D., Palm C., Peck M.C., Pohl T.M., Portetelle D., Purnelle B.,

Ramsperger U., Surzycki R., Thebault P., Vandenbol M.,

Vorhoelter F.J., Weidner S., Wells D.H., Wong K., Yeh K.-C., Batut J.;

"The composite genome of the legume symbiont Sinorhizobium meliloti.";
                                                                                                                                                                                                                                                         NCBI_TaxID=813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                084633
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
HYPOTHETICAL TRANSMEMBRANE SIGNAL PEPTIDE PROTEIN.
OrderedLocusNames=R01982; ORNAmes=SWC04336;
Rhizobium meliloti (Sinorrhizobium meliloti).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
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Q92P15;
Q1-DEC-2001
01-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61.2%;
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Pred. No. 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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            л.
Т.
                                                                                                                                                                                                                                                                                            Chlamydiaceae; Chlamydia
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        Fan J.,
J., Zhao (
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            Marathe R.,
Q., Koonin E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S., Gloux S.,
            Aravind
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J.,
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Best Local
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01-NOV-1997
01-NOV-1997
                                                                                                                                                                                                                 SGD;
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                                                                                                                                                                                                                                                                                   EMBL; U46033; AAB37236.1;
EMBL; Z74987; CAA99272.1;
EMBL; Z70678; CAA94564.1;
PIR; S66962; S66962.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (So or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
05-UUL-2004 (Rel. 44, Last annotation updat
Metal homeostasis factor ATX2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=97279235; P
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InterPro; IPR008949; Terpenoid Synth.
Pfam; PP00348; polyprenyl synt; 1.
PROSITE; PS00742; POLYPRENYL SYNTHET 1;
PROSITE; PS00444; POLYPRENYL SYNTHET 2;
COMPLETE PROCEDED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lin S.-J., Culotta V.C.;
"Suppression of oxidative damage by Saccharomyces cerevisiae which encodes a manganese-trafficking protein that localizes like vesicles";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATX2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Science 282:754-759(1998).
EMBL, AE001333; AAC68232.1;
PIR; E71491; E71491.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=97042460; PubMed=8887660;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Fungi; Ascomycota; Saccharomycotina; Sacch
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=ATX2; OrderedLocusNames=YOR079C; ORFNames=YOR29-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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GO; GO:0008299;
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S66962; Source, and interpretation of the control o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Integral membrane protein. Golgi.
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Pred. No. 1.2e+02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (See http://www.isb-sib.ch/announce/
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AAS56363;
25-MAR-2004
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Q82N27;
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Golgi sta
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01-JUN-2003 (TrEMBLrel. 24,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cerevisiae ORFs in the Gateway recombinational cloning s
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AY558037; AAS56363.1; -.
SEQUENCE 313 AA; 34408 MW; 81DAEFB0E4692268 CRC64;
                                                                                                                                     Streptomyces avermitilis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                             Putative sugar kinase.
OrderedLocusNames=SAV1476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Marsischky G., Rolfs A., Richardson A., Kane M., Baqui M., Tayche
Hu Y., Vannberg F., Weger J., Kramer J., Moreira D., Kelley F.,
Zuo D., Raphael J., Hogle C., Jepson D., Williamson J., Camargo A
Gonzaga L., Vasconcelos A.T., Simpson A., Kolodner R., Harlow E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
MEDLINE=21477403; PubMed=11572948;
Omura S., Ikeda H., Ishikawa J., H
                                       SEQUENCE FROM N.A. STRAIN=MA-4680;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Creation of the YFLEX clone resource: cloning of Saccharomyces cerevisiae ORFs in the Gateway recombinational cloning system."
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25-MAR-2004 (TrEMBLrel.
25-MAR-2004 (TrEMBLrel.
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                                                                                                NCBI_TaxID=33903;
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  Hanamoto
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  Takahashi
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Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
Racing Geffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
Racing Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
A Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
Racing F., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
Racing F., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
Racing F., Nicolski M., Oztas S., Ozier-Kalogeropoulos O.,
Racing F., Potier S., Richard G.F., Straub M.L., Suleau A.,
Racing F., Potier S., Richard G.F., Straub M.L., Suleau A.,
Racing F., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
Racing F. C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
Racing F. C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
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Racing F., Weissenbach J.,
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Best Local
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                                                                                        InterPro; Pfam; PF0
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05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
Similar to sp|(010067 Saccharomyces cerevisiae YOR079c
homeostasis factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Complete genome sequence and comparative analysis of the industrial microorganism Streptomyces avermitils."; Nat. Biotechnol. 21:526-531(2003).
EMBL, AP005027; BAC69186.1; -
GO; GC:0016301; F:kinase activity; IEA.
InterPro; IPR000600; ROK.
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Sakaki Y., Hattori M., Omura S.;
                                                                                                                            EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Candida glabrata (Yeast) (Torulopsis glabrata).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; S
Saccharomycetales; mitosporic Saccharomycetales;
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PROSITE; PS01125; ROK; 1.
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                                                                 SEQUENCE
                                                                                                                                                                   Bouchier C., Caudron B., Scarp
Wincker P., Souciet J.L.;
"Genome evolution in Yeasts.";
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                                                                                   Pro; IPR003689; Zn_transpt_Zip
PF02535; Zip; 1.
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36113 MW;
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Pred. No. 1.3e
0; Mismatches
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Score 41;
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Query Match Best Local Similarity

1.4e+02; DB 2;

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Best Local S
Matches 8
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C STRAIN=ATCC 15692 / PAO1;

C STRAIN=ATCC 15692 / PAO1;

X MEDLINE=20437337; PubMed=10984043;

X MEDLINE=20437337; PubMed=10984043;

A Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener A. Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagro A. Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan B. Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan A. Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R. Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., A. Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;

T "Complete genome sequence of Pseudomonas aeruginosa PAO1, an Opportunistic pathogen.";

Nature 406:959-964 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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PIR; D83605; D83605.

HSSP; P31133; 1A99.

GO; GO:0030288; C:periplasmic space (sensu Gr. GO; GO:0005215; F:transporter activity; IEA. GO; GO:0006810; P:transport; IEA.

InterPro; IPR006059; SBP_bac_1; Dutr-bndng.

Pfam; PF01547; SBP_bac_1; 1.
                                                                                                                                                                                                                                                                        Q74EW6 PRELIMINARY;
Q74EW6;
05-JUL-2004 (TrEMBLrel. 2
05-JUL-2004 (TrEMBLrel. 2
05-JUL-2004 (TrEMBLrel. 2
NADH oxidase, putative.
                                                                                                                                                                        Geobacter sulfurreducens.
Bacteria; Proteobacteria;
Geobacteraceae; Geobacter
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Q916G8;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Probable binding protein component of ABC transporter.
OrderedLocusNames=PA3323;
SEQUENCE FACE SERVICE STRAIN=EGA / ATCC 51573;
STRAIN=EGA / ATCC 51573;
PubMed=14671304; DOI=10.1126/science.1088727;
Marha R.A., Nelson K.E., Eisen J.A., Paulsen
                                                                                                                                                                                                                                                        ORFNames=GSU0843;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complete proteome. SEQUENCE 347 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF01547; SBP_bac_1; 1.
PRINTS; PR00909; SPERMDNBNDNG.
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Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                              NCBI_TaxID=35554;
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D.J., Lagrou M.
1 S., Yuan Y.,
K., Lim R.M.,
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Best Local S
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InterPro; IPR00103; PyrIdine_redox_2.
InterPro; IPR001100; Pyr_redox.
InterPro; IPR001100; Pyr_redox_dim.
InterPro; IPR004099; Pyr_redox_dim.
Pfam; PF00070; Pyr_redox; 1.
Pfam; PF002852; Pyr_redox; 1.
Pfam; PF002852; Pyr_redox; 1.
PRINTS; PR00369; FADBUR.
PRINTS; PR00469; PADBURASEI.
PRINTS; PR00469; PNDRDTASEI.
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02-MAR-2004
02-MAR-2004
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AAR34173;
                                                                                                                                                                                                 Methe B.A., Nelson K.E., Eisen J.A., Paulsen I.T., Nelson W.C., Heidelberg J.F., Wu D., Wu M., Ward N.L., Beanan M.J., Dodson R.J., Maddupu R., Brinkac L.M., Daugherty S.C., DeBoy R. T., Durkin A.S., Gwinn M.L., Kolonay J.F., Sullivan S.A., Haft D.H., Selengut J., Davidsen T.M., Zafar N., White O., Tran B., Romero C., Forberger H.A., Weidman J., Khouri H.M., Feldblyum T.V., Utterback T.R., Van Aken S.E., Lovley D.R., Fraser C.M.; "Genome of Geobacter sulfurreducens: metal reduction in subsurface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Heidelberg J.F., Wu D., Wu M., Ward N.L., Beanan M.J., Dodson Madupu R., Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A. Gwinn M.L., Kolonay J.F., Sullivan S.A., Haft D.H., Selengut Davidsen T.M., Zafar N., White O., Tran B., Romero C., Forber Weidman J.F., Khouri H.M., Feldblyum T.V., Utterback T.R., Van Aken S.E., Lovley D.R., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=PCA / ATCC 51573;
PubMed=14671304;
                                                                                                                          SEQUENCE
                                                                                                                                       EMBL; AE017209; AAR34173.1; TIGR; GSU0843; -.
                                                                                                                                                                        Science 302:1967-1969(2003).
                                                                                                                                                                                       environments."
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                                                                                                                                                                                                                                                                                                                                                                                                            Geobacteraceae;
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Bacteria; Proteobacteria;
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EMBL; AE017180; AAR34173.1; -.
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Pred. No.
                                                                         Score 41; DB 2;
Pred. No. 1.8e+02
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                                                                                                                          8F86F154DC054C94 CRC64;
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                                                              Mismatches
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RESULT 17 YFE9_YEAST

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Best Local
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QGFPT7;
QGFPT7;
QSFT7;
QSFT7;
QSFJUL-2004 (TrEMBLrel. 27, Created)
QSFJUL-2004 (TrEMBLrel. 27, Last sequence update)
QSFJUL-2004 (TrEMBLrel. 27, Last annotation update)
Similar to sp| P20448 Saccharomyces cerevisiae YJL033w HCA4.
ORFNames=CAGL0J01045g; /maxilaneis alahvata).
Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S., Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E., Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V. Barnay S., Blanchin S., Beckerich J.M., Beyne B., Bleykasten C., Bairsame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A., Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A., Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R., Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YFE9_YEAST STANDARD; PRT; 623 AA. P43554; O1-NOV-1995 (Rel. 32, Created) O1-NOV-1995 (Rel. 32, Last sequence update) O5-JUL-2004 (Rel. 44, Last annotation update) Hypothetical 70.3 kDa protein in ALR2-EWP47 i. OrderedLocusNames=YFL049W; Insker's vesst).
                                                                                                                                                                                                                            Candida glabrata (Yeast) (Torulopsis glabrata).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SGD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Murakami Y., Naitou M., Hagiwara H., Shibata T., Ozawa M., Sasanuma S.-I., Sasanuma M., Tsuchiya Y., Soeda E., Yokoyama Yamazaki M.-A., Tashiro H., Eki T., "Analysis of the nucleotide sequence of chromosome VI from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical SEQUENCE 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; D50617; BAA09192.1; -. PIR; S56206; S56206.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saccharomyces cerevisiae.";
Nat. Genet. 10:261-268(1995).
-i- SIMILARITY: TO YEAST NPL6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=S288c / AB972;
MEDLINE=95400292; PubMed=7670463;
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                                                                                                                                          GENOLEVURES
                                                                                                                                                          STRAIN=CBS138;
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GO:0005634; C:nucleus;
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623 AA; 7
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InterPro; IPRO01650; HeliCase_C.
InterPro; IPR001650; HeliCase_C.
Pfam; PF00270; DEAD; 1.
Pfam; PF00271; HeliCase_C; 1.
SMART; SM00487; DEXDC; 1.
SMART; SM00489; HELICC; 1.
SMART; SM00490; HELICC; 1.
PROSITE; PS00039; DEAD ATP HELICASE; UNKNOWN_1.
ATP-binding; HeliCase; Hydrolase.
SEQUENCE 765 AA; 87380 MW; A0FDB5B79E63504B
                                      MEDLINE=22206494; PubMed=12218036; Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J.D., DeBoy R.T., Dodson R.J., Gwinn M.L., Haft D.H., Hickey E.K., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L., Delcher A., Utterback T.R., Waidman J.F., Khouri H.M., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MYCTU
                                                                                                                                                                                                       Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C.M., Harris D.E., Gordon S.V., Biglmeier K., Gas S., Barry C.B. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R.M., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.D., Oliver S., Osborne J., Quall M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            996289;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence up
01-OCT-2004 (Rel. 45, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=mmpL7; OrderedLocusNames=Rv2942, ORFNames=MTCY24G1.07c;
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Bouchier C., Caudron B., Scarpelli C.,
Wincker P., Souciet J.L.;
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                                                                                                                                                                                                                                                                                                                                                                                      SPECIES=M.tuberculosis; STRAIN=H37RV; MEDLINE=98295987; PubMed=9634230; DOI=10.1038/31159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Putative membrane protein mmpL7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A., Swennene D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth Zeniou-Neyer M., Zivanovic I., Bolotin-Pukuhara M., Thierry A., Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbac
                "Whole-genome comparison laboratory strains.";
                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=1773,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Corynebacterineae; Mycobacteriaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Genome evolution in yeasts.";
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   184:5479-5490(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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                                of Mycobacterium tuberculosis
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Q7NJE3;
Q1-MAR-2004
01-MAR-2004
01-MAR-2004
MEDLINE-22977040, PubMed=14621292;
Nakamura Y., Kaneko T., Sato S., Mimuro M., Miyashita H., Tsuchiya Sasamoto S., Watanabe A., Kawashima K., Kishida Y., Kiyokawa C., Kohara M., Matsunoto M., Matsuno A., Nakazaki N., Shimpo S., Takeuchi C., Yamada M., Tabata S.;
                                                                                                                         SEQUENCE FROM N.A. STRAIN=PCC 7421;
                                                                                                                                                                                                   Gloeobacter violaceus.
Bacteria; Cyanobacteria; Chroococcales;
                                                                                                                                                                                                                                                   OrderedLocusNames=gll1889;
                                                                                                                                                                                                                                                                        Gll1889 protein.
                                                                                                                                                                                       NCBI_TaxID=33072;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; BX842581; CAB06107.1; -. EMBL; AE007123; AAK47339.1; -. EMBL; BX248344; CAD96654.1; -. EMBL; C70668; C70668.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansor H., Pryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S., Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R., Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G., "The complete genome sequence of Mycobacterium bovis.", Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882 (2003).

1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR004869; MMPL.
Pfam; PF03176; MMPL; 1.
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SPECIES=M.Dovis; STRAIN=AF2122/97;

MEDLINE=22709107; PubMed=12788972; DOI=10.1073/pnas.1130426100;

Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H.,

Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H.,

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Pred. No. 3.5e+02;
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QBHG38;

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Translation
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EMBL; AP006574; BAC89330.1; - GO; GO:0005871; C:kinesin complex; IBA.

GO; GO:000377; F:microtubule motor activ InterPro; IPR002151; Kinesin_light.

InterPro; IPR001440; TPR.
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Q6L0E6;
05-JUL-2004
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SEQUENCE FROM N.A.

Wu X., Wang Y., Zhou K., Zhu W., Nie J., Wang C., Xie W.,
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

EMBL, AF511507; AAN84928.1; -.

GO; GO:0005739; C:mitochondrion; IEA.

GO; GO:0005137; F:NADH dehydrogenase (ubiquinone) activity;

GO; GO:0006120; P:mitochondrial electron transport, NADH to
InterPro; IPR001457; Oxidored q3.

Pfam; PF00499; Oxidored q3; 1.
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InterPro; IPR00140; TPR.
Pfam; PF00515; TPR; 9.
PRINTS; PR00381; KINESINLIGHT.
PR051TE; PS50005; TPR; 6.
PR0SITE; PS50293; TPR_REGION; 1.
Complete proteome.
SEQUENCE 999 AA; 109847 MW; ED
NCBI_TaxID=82076;
                                                                  Archaea; Euryarchaeota; Ther
Picrophilaceae; Picrophilus.
                                                                                                                                                          OrderedLocusNames=PTO0971;
Picrophilus torridus.
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SEQUENCE 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21
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9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FGSGLVVVEGGSFM
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8; Conserv
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4 (TrEMBLrel. 27, Las
4 (TrEMBLrel. 27, Las
6 (TremBLrel. 27, Las
7 initiation factor 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA; 18603 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Chinese alligator)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61.2%;
                                                                                                     Thermoplasmata;
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, Last anno
tor 2 beta
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 40; DB 2;
Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51012386670F4AF3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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                                                                                                                                                                                                                                                                sequence update) annotation updat
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                                                                                            Thermoplasmatales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .7e+02;
                                                                                                                                                                                                                                                                update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCC 7421,
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                                                                                                    RX MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Distchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Distchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Distchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Richards S., McCEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Pahey J., Helton E., Kettenan M., Madan A., Rodrigues S., Sanchez A.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Jones S.J. Masyra M.A.,

RA Jones S.J. Manyra M.A.
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Best Local S
Matches
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Q7ZSZ2;
Q1-UN-2003 (TrEMBLrel. 24, Created)
Q1-JUN-2003 (TrEMBLrel. 24, Last sequence update)
Q5-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Gene exp
Claudin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ProDom; PD004078; eIF5_eIF2B; 1.

SMART; SM00653; eIF2B 5; 1.

PROSITE; PS50926; TRAM; 1.

Complete proteome; Initiation factor.

Complete proteome; Initiation factor.
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EMBL; AE017261; AAT43556.1; -
GO; GO:0003743; F:translation initiation factor a
InterPro; IPR002735; eIF5 eIF2B.
InterPro; IPR002792; TRAM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. Fujita M., Itoh M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Ver
Amphibia; Batrachia; Anura; Mesobatrachia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=cldn7L1;
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Pfam; PF01938; TRAM; 1.
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Schepers B., Dock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N. STRAIN=DSM 9790 PubMed=15184674;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xenopus laevis (African clawed
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Schepers B., Dock C., Antranikian G., Li
"Genome sequence of Picrophilus torridus
                                                                                       Jones S.J., Marra
                                                        'Generation and initial analysis of more than 15,000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23
mouse cDNA sequences.";
c. Natl. Acad. Sci. U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a M., Itoh M., Shibata M., Taira S., Taira M., expression pattern analysis of the tight junctin, in the early morphogenesis of Xenopus embr. Expr. Patterns 2:23-26(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66
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9790 / ATCC 700027;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59.7%;
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Pred. No.
   99:16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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Liebl W.;
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3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    factor activity; IEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           junction protein, embryos.";
                                                        full-length
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Best Local S
Matches
                                                                                    [1]
SEQUENCE FROM N.A.
MEDLINE=93099269; PubMed=1463852;
Niehaus A., Gisselmann G., Schwenn J.D.;
Niehaus erructure of the Synechococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q55309; Q935X7;
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Phosphoadenosine phosphosulfate reductase (EC 1.8.4.8) (PAI
reductase, thioredoxin dependent) (PAdoPS reductase) (3'-
phosphoadenylylsulfate reductase) (PAPS sulfotransferase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SYNP7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Klein S., Strausberg R.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ
EMBL; AB072910; BAC21015.1; -.
EMBL; BC048771; AA448771.1; -.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0005923; C:tight junction; IEA.
GO; GO:0005923; F:structural molecule activity
GO; GO:0005198; F:structural molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR006187; Claudin.
InterPro; IPR003552; Claudin7.
InterPro; IPR006188; Claudin reg.
InterPro; IPR004031; PMP22 Claudin.
Pfam; PF00822; PMP22 Claudin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [3]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=cysH; Synonyms=par, sea0019;
Synechococcus sp. (strain PCC 7942) (Anacystis nidulans
Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transmembrane.
                                                                                                                                                                                                                Holtman C.K.,
                                                                                                                                                                                                                                        SEQUENCE FROM
                                                                                                                                                                                                                                                                                    "Primary structure gene.";
Plant Mol. Biol. 20
                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=1140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYSH_SYNP7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS01346; CLAUDIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PRO1077; CLAUDIN. PRINTS; PRO1381; CLAUDIN7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        initiative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Richardson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Klein S.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=22341132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FISSUE=Embryo;
                                                                                                                                                                                                                                                                                  ant Mol. Biol. 20:1179-1183(1992).
branch; third step.
SUBCELLULAR LOCATION: Cytoplasmic (By similarity)
SIMILARITY: Belongs to the PAPS reductase family.
                                                                  PATHWAY: Sulfate activation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dyn.
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9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ve.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EFGAGLVLG--GQFM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genomic tools for Xenopus research:
                                                                                                                                                                                                                M N.A.
, Socias T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AΑ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59.7%;
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                                                                                                                                                                                                                  Mohler B.J.,
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      the PAPS reductase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 40; DB
Pred. No. 1.4e
2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDDF3E2D804B5775 CRC64;
                                                                  cysteine biosynthesis
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                                                                                                                                                                                                                      Chen Y.,
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2;
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                                                                                                                                                                                                                      Min H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IEA.
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        CysH subfamily.
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                                                                      reductive
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RESULT 25
Q8KMM1
ID Q8KMM
AC Q8KMM
AC Q8KMM
AC Q8KMM
DT 01-MA
DT 00-MA
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DT 00-MA
DT 01-MA
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  RESULT 26
CAD24411
ID CAD24
AC CAD24
DT 12-MA
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Matches 8
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Best Local
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EMBL; U3052; AAL03931.1; -.
PIR; S28609; S28609.
HSSP; P17854; ISUR.
HAMAP; MF 00063; -; 1.
InterPro; IPR004511; cysH.
InterPro; IPR004511; cysH.
InterPro; IPR004511; cysH.
InterPro; IPR004511; cysH; 1.
TIGRPAMS; TIGR00434; cysH; 1.
TIGRPAMS; TIGR00434; cysH; 1.
Cysteine biosynthesis; Oxidoreductase.
CONFLICT 218 218 T -> S (in Ref. 2)
CAD24411;
CAD24411;
12-MAY-2004
12-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q8KMM1;
Q8KMM1;
01-OCT-2002
01-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q8KMM1;
01-OCT-2002 (TrEMBLrel. 22, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Helanto M.E.K., Airaksinen U., von Weymarn N., Submitted (FEB-2002) to the EMBL/GenBank/DDBJ of EMBL; AJ431694; CAD24411.4; -... GO; GO:0008865; F:fructokinase activity; IEA. GO; GO:0016301; F:kinase activity; IEA. GO; GO:0016740; F:transferase activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long; modified and this statement is not removed; entitles requires a license agreement (See lor send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00480; ROK; 1.
PROSITE; PS01125; ROK; UNKNOWN_1.
Kinase; Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Leuconostoc pseudomesenteroides.
Bacteria; Firmicutes; Lactobacil
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=ATTC-12291;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=33968;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000600;
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                                                                                                                                                                                                                                                                                          Similarity 7; Conserv
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8; Conserv
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GAGIVSGGRFV 146
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                                                                                                                                                                                                                                                                                                                                                                                             288 AA;
                                                                                                                                                                                                                                                                                               Conservative
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(TrEMBLrel.
                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                    59.7%;
63.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ROK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26636 MW;
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27,
27,
Created)
Last sequence update)
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Pred. No. 1.5e+02;
                                                                                                                                                                                                                                                                                                                      Pred.
                                                                                                                                                                                                                                                                                                                                           Score 40; DB 2;
                                                                       PRT;
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RESULT 28
FABH_TROWT
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Best Local S
Matches 7
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O1-JAN-1998 (TrEMBLrel. 05, Cre. O1-JAN-1998 (TrEMBLrel. 05, Las O1-JUN-2003 (TrEMBLrel. 24, Las Putative rhamnosyl transferase.
                                                                                       FABH TROWT STANDARD; PRT; (2031L5; Q03N01; C0-COT-2003 (Rel. 42, Created) 10-CCT-2003 (Rel. 42, Last sequence upon the company of the company
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001173; Glyco_trans_2.
InterPro; IPR00446; Rhammosyltran.
Pfam; PF00535; Glycos transf_2; 1.
TIGRPAMs; TIGR01556; Thamnosyltran;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jedani K.E., Stroeher U.H., Manning P.A.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ
EMBL; AF025396; AAB81635.1; -.
GO; GO:0016740; F:transferase activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mannitol production.";
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases
EMBL; AJ431694; CAD24411.4; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=ATTC-12291;
Helanto M.E.K., Airaksinen U., von
"Characterization of random mutant
                        3-oxoacyl-[acyl-carrier-protein] synthase III ketoacyl-ACP synthase III) (KAS III)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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STRAIN=85-3954-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=55601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria, Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Listonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vibrio anguillarum (Listonella anguillarum)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=orf33x8;
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OrderedLocusNames=TWT253
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irmicutes; Lactobacillales;
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63.6%;
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    27, Last annotation update)
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                                                                                                                             update)
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                                                              2.3.1.41) (Beta-
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Query Match
Best Local S
Matches 8
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Bentley S.D., Malwald M., Murphy L.D., Pallen M.J., Yeats C.A.,
Dover L.G., Norbertczak H.T., Besra G.S., Quail M.A., Harris D.F
von Herbay A., Goble A., Rutter S., Squares R., Squares S.,
Barrell B.G., Parkhill J., Relman D.A.;
"Sequencing and analysis of the genome of the Whipple's disease
bacterium Tropheryma whipplei.";
Lancet 361.637-644(2003).
1- FUNCTION: Catalyzes the condensation reaction which
synthesis by the addition to an acyl acceptor of two carbons
malonyl-ACP. Catalyzes the first condensation reaction which
                                                                                                                                                                                                                                                                                                       InterPro;
TIGRFAMs;
                                                                                                                                                                                                                                                                                                                                              EMBL; AE016851; AA044350.1; ALT_INIT.
EMBL; BX251411; CAD67184.1; -.
HSSP; O06399; 1HZP.
HAMAP; MF_01815; -; 1.
                                                                                                                                                                                                              ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (See http:\overline{//www}.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                         Acyltransferase; Complete proteome; Multifunctional enzyme; Transferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This
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MEDLINE=22784088; PubMed=12902375;
Raoult D., Ogata H., Audic S., Robe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   similarity).
SIMILARITY: Belongs to the fabH family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [acyl-carrier protein].

PATHWAY: Fatty acid biosynthesis.

SUBUNIT: Homodimer (By similarity).

SUBCELLULAR LOCATION: Cytoplasmic (Probable).

DOMAIN: The last Arg residue of the ACP-binding sit for the weak association between ACP/acpP and fabH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         initiates fatty acid synthesis and may therefore play a role in governing the total rate of fatty acid production. Possesses botl acetoacetyl-ACP synthase and acetyl transacylase activities. Its substrate specificity determines the biosynthesis of branched-chain and/or straight-chain of fatty acids (By similarity). CATALYTIC ACTIVITY: Acyl-[acyl-carrier protein] + malonyl-[acyl-carrier protein] + CO(2) +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SWISS-PROT entry is copyright. It is produced through en the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Res. 13:1800-1809(2003)
                                                                      Similarity
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FGAGLVLGGQ
                                                                                                                                                                                                                                                                                                     IPR004655; FabH synth.
TIGR00747; fabH; 1.
                                                                                                                                            278
248
322 J
                                                Conservative
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11
                                                                                                                                          34211
                                                                      59.7%;
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                                    Score 40; us a Pred. No. 2e+0; O; Mismatches
                                                                                                                                     By similarity.
By similarity.
By similarity.
By similarity.
ACP-binding (By similarity).
, 3A2A1E592BDF1804 CRC64;
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                                                                                                                                                                                                                                                                                 Fatty acid
                                                                      2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Usage
                                                                                         Length 322;
                                                                                                                                                                                                                                                                                 biosynthesis;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Mus musculus 9.5 days embryo parthenogenote cDNA, RIKEN full-length
enriched library, clone:B130020M16 product:DEAD/H (Asp-Glu-Ala-
Asp/His) box polypeptide 10 (RNA helicase), full insert sequence.
                                                                                                                                                                                                                                                                                                      Shibata K.. Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P. Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watshiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J. Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; RIKEN integrated sequence analysis (RISA) system-394-format sequencing pipeline with 384 multicapillary sequencer."; Genome Res. 10:1757-1771(2000).
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STRAIN=CS7BL/6J; TISSUE=Parthenogenote;
STRAIN=CS9279253; PubMed=10349636;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length CDNA cloning.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q8BRE3;
01-MAR-2003
Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirzozane T., Hirzozane T., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T., Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya Kurihara C., Matenuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shiba Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y., "Normalization and subtraction of cap-trapper-selected prepare full-length cDNA libraries for rapid discovery Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Parthenogenote;
MEDLINE=20499374; PubMed=11042159;
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the RIKEN Genome Exploration Research Group
"Analysis of the mouse transcriptome based o
60,770 full-length cDNAs.";
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STRAIN=C57BL/6J; TISSUE=Parthenogenote;
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STRAIN=C57BL/6J; TISSUE=Parthenogenote;
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Mammalia; Eutheria;
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STRAIN=C57BL/6J; TISSUE=Parthenogenote;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Functional annotation of a full-length mouse cDNA collection.";
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Rodentia;
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on functional
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R GO; GO:0005524; F:ATP binding; IEA.
R GO; GO:0008026; F:ATP-dependent helicase activity; IEA.
R GO; GO:0016787; F:hydrolase activity; IEA.
R GO; GO:0016787; F:hydrolase activity; IEA.
R InterPro; IPR001410; DEAD;
R InterPro; IPR001545; DEAD/DEAH_N.
R InterPro; IPR001559; DEAD/DEAH_N.
R InterPro; IPR001659; DEAD/DEAH_S.
R InterPro; IPR001659; Helicase_C.
R Ffam; PF00270; DEAD; 1.
R Pfam; PF00271; Helicase_C; 1.
R Pfam; PF00271; Helicase_C; 1.
R SMART; SM00487; DEXDC; 1.
R SMART; SM00487; DEXDC; 1.
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SIMILARITY: Belongs to the DEAD box helicase family.

EMBL, AK045032, BAC32191.1; -.
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Q9A7D4; PT (TEMBLEE 1. 17, Created)
01-JUN-2001 (TEMBLEE 1. 17, Last sequence update)
01-JUN-2003 (TEMBLEE 1. 24, Last annotation update)
Hypothetical protean CCT789.
OrderedLocusNames=CCT89;
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ATP-binding; Helicase; Hydrolase.
NON_TER 462
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SIRAINS-ATCC 19089 / CB15;
MEDLINE-21173698; PubMed=11259647; DOI=10.1073/pnas.061029298;
MEDLINE-21173698; PubMed=11259647; DOI=10.1073/pnas.061029298;
MEDLINE-21173698; PubMed=11259647; DOI=10.1073/pnas.061029298;
MEDLINE-21173698; PubMed=11259647; DOISON K.E., Paulsen I.T., Nelson W.C., Laub M.R.K., Ohta N., Maddock J.R.,
Eisen J.A., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
Dotscka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
Kolonay J.F., Smit J., Craven M.B., Khouri H.M., Shetty J.,
Berry K.J., Utterback T.R., Tran K., Wolf A.M., Vamathevan J.J.,
Ermolaeva M.D., White O., Salzberg S.L., Venter J.C., Shapiro L.,
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Proc. Natl. Acad. Sci. U.S.A. 98:4136-414
EMBL; AE005853; AAK23765.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                       raser C.M.;
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Pred. No.
                                                                                             Score 40; DB
Pred. No. 2.9e
1; Mismatches
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red. No. 2.8e+02;
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1AC43E2A90950D5A CRC64;
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PubMed=15001715;

Dietrich F.S., Voegeli S., Brachat S
Mohr C., Pohlmann R., Luedi P., Choi
Gaffney T.D., Philippsen P.;

"The Ashbya gossypii genome as a too
Saccharomyces cerevisiae genome.";
Science 304:304-307(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q754E9;
Q754E9;
05-JUL-2004
05-JUL-2004
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23-APR-2004
23-APR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ashbya gossypii (Yeast) (Eremothecium gossypii).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Eremothecium.
                                                                                                                                                                                                                                         AFR121Wp.
AFR121W.
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Mohr C., Pohlmann R., Luedi P.,
Gaffney T.D., Philippsen P.;
"The Ashbya gossypii genome as a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN=ATCC 10895;
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                                                                                                                                                                                                          Ashbya gossypii (Yeast) (Eremothecium gossypii).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Eremothecium.
                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE016901; AAS53492.1; -. AGD; AFR121W; -.
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Science 304:304-307(2004).
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PubMed=15001715;
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                                                                            EMBL; AE016901; AAS53492.1; -. SEQUENCE 555 AA; 65009 MW;
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                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 _TaxID=33169;
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., Wing R.A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                Length 555
                                                             Length 555;
                                                                                                                                                                                                                                                                                                                                                                                                                                       CRC64;
                                                                                                                                           A., Flavier
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                                            Gaps
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RESULT 34
Q7TMM1
ID Q7TMM
AC Q7TMM
DT 01-OC
DT 01-MA
DE Ddx10
GN Numer
OC Eukar
OC Mamma
OC MAmma
OC MCBI
RP SEQUE
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Q9KPJ7
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Best Local S
Matches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00990; GGDEF; 1.
Pfam; PF00785; PAC; 1.
SMART; SM00267; DUF1; 1.
SWART; SM00086; PAC; 2.
SMART; SM00091; PAS; 2.
TIGRPAMM; TIGR00254; GGDEF; 1.
TIGRPAMM; TIGR00229; Sensory_boy
PROSITE; PS50887; GGDEF; 1.
PROSITE; PS50813; PAC; 2.
                                                                                                                                                                                Q7TMM1;
Q7TMM1;
01-OCT-2003 (TrEMBLrel. 25,
01-OCT-2003 (TrEMBLrel. 25,
01-MRR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9KPJ7;
01-OCT-2000
01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TIGR; VC2370; -.
GO; GO:000155; F:two-component sensor molecule activity;
GO; GO:0000160; P:two-component signal transduction system
InterPro; IPR000160; GGDEF.
InterPro; IPR001610; PAC.
InterPro; IPR001014; PAS.
InterPro; IPR000700; PAS-assoc_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

STRAINEI TOR N16961 / Serotype O1;

MEDLINE=20406833; PubMed=10952301; DOI=10.1038/35020000;

Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.I.

Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,

Edill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.L.,

Ermolaeva M.D., Vamathevan J.J., Bass S., Qin H., Dragoi I.,

Sellers P., McDonald L.A., Utterback T.R., Fleischmann R.D.,

Nierman W.C., White O., Salzberg S.L., Smith H.O., Colwell R.R.,

Mekalanos J.J., Venter J.C., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-MAR-2004 (TrEMBLrel. 26, Sensory box/GGDEF family proproceduccusNames=VC2370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Vibrio.
SEQUENCE FROM N.A
                                                                                                                                        Ddx10 protein (Fragment)
Name=Ddx10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 406:477-483(2000).
EMBL; AE004307; AAF95513.1;
PIR; B82085; B82085.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vibrio cholerae.
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                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                    Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=666;
                                          NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "DNA sequence of both
                                                                                                                                                                                                                                                                                                                                                                                                              13
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8; Conserv
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579 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Å.
                                                                                                                                                                                                                                                                                                                                                                                                              21
                                                                      Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65762 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59.7%;
88.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         r J.C., Fraser C.M.; chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein.
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Last
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Pred. No.
                                                                    Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6E37C8B467A46CD6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.4e+02;
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RESULT
Q8C751
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DT 01
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XX MEDLINE-22380257; PubMed=12477932;

XX MEDLINE-22380257; PubMed=12477932;

XX MEDLINE-22380257; PubMed=12477932;

XX MEDLINE-2380257; PubMed=12477932;

XX Altschul S.F., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

XX Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

XX Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

XX Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,

XX Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

XX Altschul S.F., Jordan H., Moore T., Casavant T.L., Scheetz T.E.,

XX Stepleton M., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,

XX Stepleton M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,

XX Brownstein M.J., Wadin T.B., Toshiyuki S., Carninci P., Prange C.,

XX Brownstein M.J., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

XX Alas S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

XX Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Hullahy S.J.,

XX Allalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

XX Allalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

XX Allalon D.K., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

XX Milting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

XX Milting M., Madan A., Tonehan J.W., Green E.D., Dickson M.C.,

XX Allakesley R.W., Turkinan M., Schmutz J., Myers R.M., Butterfield Y.S.,

XX Jones S.J., Marra M.A.,

XX Jones 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local s
Matches 6
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InterPro; IPR001545; DEAD/DEAH N.
InterPro; IPR001629; DEAD box.
InterPro; IPR001650; Helicase_C.
InterPro; IPR001650; Helicase_C.
Pfam; PF00270; DEAD; 1.
Pfam; PF00271; Helicase_C; 1.
SMART; SM00480; HELICC; 1.
SMART; SM00490; HELICC; 1.
PROSITE; PS00039; DEAD ATP HELICASE; 1.
ATP-binding; Helicase; Hydrolase.
NON TER
623
623
623
                                                                                                                                                                                                                                                                                                                                                                                                                                             Q8C751,
                                                                                                                            01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Mus musculus 13 days embryo lung cDNA, RIKEN full-length enriched
library, clone:D430047D13 product:DEAD/H (Asp-Glu-Ala-Asp/His) box
polypeptide 10 (RNA helicase), full insert sequence. (Fragment)
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EMBL; BC055481; AAH55481.1; -.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0008026; F:ATP-dependent helicase activity;
GO; GO:0016787; F:hydrolase activity; IEA.
GO; GO:0003676; F:nucleic acid binding; IEA.
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                             Name=Ddx10;
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     Eukaryota; Metazoa;
                                                   Mus musculus (Mouse)
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6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         623 AA;
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     Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70849 MW; F5B6893E71179D94 CRC64;
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Pred. No. 3.6e+02;
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PRESENTATION OF CREATER AND REPORT OF CREATE
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ESEQUENCE FROM N.A.

C STRAIN=C57BL/6J; TISSUE=Lung;

C STRAIN=C9530913; PubMed=11076861;

MEDLINE=20530913; PubMed=1
                                                                                                                                                                             C STRAIN-GS7BL/GJ; TISSUB-Lung;

RC STRAIN-GS7BL/GJ; TISSUB-Lung;

RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,

RA Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W.,

Ra Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,

RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,

RA Katch H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,

RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,

RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohnato N., Okazaki Y.,

RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohnato N., Okazaki Y.,

RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,

RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,

RA Sasaki D., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,

ROMATU A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;

RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;

RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;

RA TOMATU A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;

RA TOMATU A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;

RA TOMATU A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;

RA TOMATU A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;

RA TOMATU A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;

RA TOMATU A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;

RA TOMATU A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;

RA TOMATU A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;

RA TOMATU A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;

RA TOMATU A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;

RA TOMATU A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;

RA TOMATU A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;

RA TOMATU A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;

RA TOMATU A., Toya T., Yasunishi A., Muramatsu M., Muramatsu M.,

RA TOMATU A., Toya T., Yasunishi A., Muramatsu M., Muramatsu M.,

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MEDLINE=99279253; PubMed=10349636;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
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MEDLINE=21085660; PubMed=11217851;
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                                                                                                      InterPro;
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                                                             IPR011545;
IPR000629;
                                                                                                                                                         IPR001410; DEAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rodentia;
          DEAD/DEAH_N.
DEAD_box.
Helicase_C.
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QRESULT QRECESS IN CONTROL OF CON
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RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carrinci P., Frange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carrinci P., Frange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carrinci P., Frange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., WcDley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., WcDley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Millano D.K., Toung A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Rodriguez S.T. Malek U., Smailus D.E., Schnerch A., Schein J.E.,
RA Rodriguez S.T. Malek U., Smailus D.E., Schnerch A., Schein J.E.,
RA Rodriguez S.T. Malek U., Smailus D.E., Schnerch A., Schein J.E.,
RA Rodriguez S.T. Malek U., Smailus D.E., Schnerch A., Schein J.E.,
RA Rodriguez S.T. Malek U., Smailus D.E., Schnerch A., Schein J.E.,
RA Rodriguez S.T. Malek U., Smailus D.E., Schnerch A., Schein J.E.,
RA Rodriguez S.T. Malek U., Smailus D.E., Schnerch A., Schein J.E.,
RA Rodriguez S.T. Malek U., Smailus D.E., Schnerch A., Schein J.E.,
RA Rodriguez S.T. Malek U., Smailus D.E., Schnerch A., Schein J.E.,
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Best Local S
Matches 6
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pfam; PF00271; Helicase C; 1.
SMART; SM00487; DEXDC; 1.
SMART; SM00490; HELICC; 1.
PROSITE; PS00039; DEAD ATP HELICASE; 1.
ATP-binding; Helicase; Hydrolase.
NON_TER 681 681
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01-MAR-2003 (TrEMBLrel. 23,
01-MAR-2004 (TrEMBLrel. 26,
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                                                                                                                                                                                           Strausberg R.;
Strausberg R.;
Strausberg Fiber 2002) to the EMBL/GenBank/DDBJ databases
submitted (FEB-2002) to the DEAD box helicase family
1- SIMILARITY: Belongs to the DEAD box helicase family
EMBL; BC023303; AAH23303:1; --
HSSP; P10081; 10VA.
MGD; MGI:1924841; Ddx10.
MGD; MGI:1924841; Ddx10.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0005524; F:ATP-dependent helicase activity; IEA.
GO; GO:0016787; F:hydrolase activity; IEA.
GO; GO:0016787; F:hydrolase activity; IEA.
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jones S.J., Marra M.A.;
Jones S.J., Marra M.A.;
"Generation and initial analysis of more than 15,000
and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=22388257; PubMed=12477932;
           30; GO:000030; DEAD.
InterPro; IPR011545; DEAD/DEAH N.
InterPro; IPR010629; DEAD_DOX.
InterPro; IPR010629; Helicase_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Eye;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                         30; GO:0003676; F:nucleic acid binding;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FROM N.A.
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Last annotation update)
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Pred. No. 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren S.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
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Best Local Similarity
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01-JUN-2003
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISUE=Lymph;
MEDLINE=22388257; PubMed=12477932;
MEDLINE=22388257; PubMed=12477932;
Median R.L., Feingold E.A., Grouse L.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q86VR6;
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SMART; SM00487; DEXDC; T.
SMART; SM00490; HELICG; 1.
PROSITE; PS00039; DEAD_ATP_HELICASE; 1.
ATP-binding; Helicase; Hydrolase.
NON_TER_ 681 681
      Pfam; PF00270; DEAD;
Pfam; PF00271; Helica
SMART; SM00487; DEXD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                            and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                     Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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7; DEXDc; 1.
0; HELICc; 1.
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Last annotation updat
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Pred. No. 3.9e+02;
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RESULT OF CONTROL OF C
                                                                                                          RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Estans C.A., Golayne J.D.,
RA Mannatidee P.G., Scherer S.E., Holt R.A.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Champe M., Pfeiffer B.D.,
RA Batton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Man K.H., Doyle C., Baxter B.G., Champe M., Pfeiffer B.D.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxtendale J., Bayraktaroglu L., Beasley E.M.,
RA Below R.W., Basu A., Batter H., Cadieu E., Center A., Chandra I.,
RA Ghory J.M., Cawley S., Dahlke C., Davenport L.B., Davise P.,
RA Ghory J.M., Cawley S., Dahlke C., Davenport L.B., Davise P.,
RA Ghori S., Calbard R., Chandra I.,
RA Gerblos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Glodk R., Goup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Glodk R., Gong F., Gorrell J.H., Glasser K.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Liasko P., Lei Y., Levitsky A.A., Li J., Li J.,
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Matches 6
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Q9VX34;
Q9VX34;
01-MAY-2000
01-OCT-2002
05-JUL-2004
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ATP-binding; Helicase; HydTolase.
NON_TER 745 745
SEQUENCE 745 AA; 85831 MW; F689AC
SEQUENCE FROM N.A.
MEDLINE=22426065; PubMed=12537568;
Celniker S.E., Wheeler D.A., Kronm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CG5800-PA (RE19835p).
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69 DFSAGLIIGGK 179
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22,
27,
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Last annotation update)
   Kronmiller B.,
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Pred. No.
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      Carlson J.W., Halpern
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Yao Q.A., Ye J.,
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Fleischmann W.,
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                                                                                                                                                                                                                        Smith H.O.
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                                                                                                                                                                                                                                                 InterPro; IPR001410; DEAD.
InterPro; IPR001545; DEAD/DEAH N.
InterPro; IPR001629; DEAD/DOX.
InterPro; IPR001650; Helicase_C.
Pfam; PF00270; DEAD; 1.
Pfam; PF00271; Helicase_C.
Pfam; PF00271; Helicase_C.
SMART; SM00489; DEXDC; 1.
SMART; SM00490; HELICC; 1.
SMART; SM00490; HELICC; 1.
SMART; SM00490; DEAD_ATP_HELICASE; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frik George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liac Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Misra S., Crosby M.A., Mungall C.J., Millburn G.H., Prochnik S.E.
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.
Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P
Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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Kaminker J.S., Bergman C.M., Kronmiller
Patel S., Frise E., Wheeler D.A., Lewis
Ashburner M., Celniker S.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The transposable elements of the Drosophila melanogaster euchromatin: a genomics perspective.";
Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Celniker S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FLYBASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Annotation of the Drosophila melanogaster euchromatic genome: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lewis S.E.;
                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                         PROSITE; PS00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FlyBase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Base; FBgn0030855; CG5800.
GC:0005524; F:ATP binding; IEA.
GC:0008026; F:ATP-dependent helicase activity;
GO:0003676; F:nucleic acid binding; IEA.
                             Н
                                                                                   6; Conserv
EFGAGLVLGGQ 11 : | | | | : : | | :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MAR-2004)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3:RESEARCH0083-RESEARCH0083 (2002)
                                                                                      Conservative
                                                                                                                                                                                                                               Helicase; Hydrolase
                                                                                                                                                                                                    AA;
                                                                                                                                                                                                    92844 MW;
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                                                                                                              59.7%;
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                                                                          Pred. No. 3.004; Mismatches
                                                                                                                 Score 40;
Pred. No.
                                                                                                                                                                                                       92A2897054268066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B., C
                                                                                                                                               DB 2;
                                                                                                                 ,6e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               databases
                                                                                                                                            Length 826;
                                                                                                                                                                                                       CRC64;
                                                                                         Indels
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., Park S.,
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Query Match
Best Local S
Matches 6
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Pfam; PF00271; Helicase C; 1.

SMART; SM00487; DEXDC; 1.

SMART; SM00489; HELICC; 1.

SMART; SM00490; HELICC; 1.

SMART; SM00490; HELICASE; 1.

PROSITE; PS00039; DEAD ATP HELICASE; 1.

PROSITE; PS00039; DEAD ATP HELICASE; 1.

ATP-binding; Helicase; RNA-binding;

NP_BIND 113 120 NEAD POX.

SITE 222 225

CONFLICT 647 647 A -> D (in Reconstition of the constitution of the constitut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arai Y., Kaneko Y., Kubo T., Arai K., Hosoda F., Ohki M.;
"Molecular analysis of the chromosomal breakpoints and id
of the repetitive sequences near the breakpoints of NUP98
related leukemia with inv(1)(p15q22).";
Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
-!- FUNCTION: Putative ATP-dependent RNA helicase.
-!- TISSUE SPECIFICITY: High in testis but widely express
-!- SIMILARITY: Belongs to the DEAD box helicase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HUMAN
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MEDLINE=96301396; PubMed=8660968;

MEDLINE=96301396; PubMed=8660968;

Savitsky K., Ziv Y., Bar-Shira A., Gila

Uziel T., Sfez S., Nahmias J., Sartiel

Collins F.S., Shiloh Y., Rotman G.;
                                                                                                                         CONFLICT
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
EMBL;
HSSP;
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Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUL-1998 (Rel. 36, I
05-JUL-2004 (Rel. 44, I
Probable ATP-dependent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MIM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AB040537; BAB18536.1; -. HSSP; P10081; 1QVA. SWISS-2DPAGE; Q13206; HUMAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. Arai Y., Kaneko Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genomics 33:199-206(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "A human gene (DDX10) encoding a putative DEAD-box RNA helicase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO; GO:0003724; F:RNA helicase
InterPro; IPR001410; DEAD.
InterPro; IPR000629; DEAD box.
InterPro; IPR001650; HeliCase_(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11q22-q23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genew; HGNC:2735;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.; WWW="http://www.infobiogen.fr/services/chromcancer/Genes/DDX10.html".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAMUH
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   Similarity 6; Conserv
                                                                                                                         113
222
647
658
661
875
      Conservative
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100815
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Primates;
                                59.7%;
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Last annotation update)
t RNA helicase DDX10 (DEAD-box protein 10).
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      Score 40; DB
Pred. No. 4.9e
4; Mismatches
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D -> E (in
N -> K (in
      4;
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Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                             -> D (in Ref. 2).
-> E (in Ref. 2).
-> K (in Ref. 2).
4692EDA56AD945B5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             activity;
                                                                                                                                                                                                                                                                                           (Potential)
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                                          .9e+02;
                                                              Length 875;
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                                                                                                                                   CRC64;
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d identification
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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altechul S.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Schibbs R.A.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Solbs R.A.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Butterfield C.G.,
RA Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Willialon D.K., Wong A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
                                                                                               Query Match
Best Local Similarity
                                                                     Matches
                                                                                                                                                                                                                                       InterPro; IPR001410; DEAD.
InterPro; IPR001545; DEAD/DEAH N.
InterPro; IPR001545; DEAD/DEAT.
InterPro; IPR001629; DEAD_Dox.
InterPro; IPR00150; Helicase_C.
Pfam; PF00270; DEAD; 1.
Pfam; PF00271; Helicase_C; 1.
SMART; SM00487; DEXDC; 1.
SMART; SM00480; HELICG; 1.
SMART; SM00490; HELICG; 1.
PROSITE; PS00039; DEAD_ATP_HELICASE; 1.
ATP-binding; Helicase; Hydrolase.
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01-JUN-2003 (TrEMBLrel. 24,
01-JUN-2003 (TrEMBLrel. 24,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
Submitted (MAR-2003) to the DEAD box helicase family.
I SIMILARITY: Belongs to the DEAD box helicase family.
EMBL; BC049261; AAH49261.1; -.
EMBL; BC049261; AAH49261.1; -.
EMBL; BC049261; Ddx10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0008026; F:ATP-dependent helicase activity; IEA.
GO; GO:0016787; F:hydrolase activity; IEA.
GO; GO:0003676; F:nucleic acid binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q80Y44
                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jones S.J., Marra M.A.;
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EFGAGLVLGGQ 11
                                                                                                                                                                                                             891 AA; 102289 MW; FCCABEEFA9FA5892 CRC64;
                                                                     Conservative
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                                                                                               59.7%; Score 40; DB 2; 54.5%; Pred. No. 5e+02;
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    Mismatches

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Search completed: December 9, 2004, 09:20:51 Job time : 9.96223 secs

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Result
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1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/1aa/backfIles1.pep:*
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US-09-215-212-12
US-09-215-212-13
US-09-252-991A-27542
US-09-252-991A-23724
US-09-252-991A-23386
US-09-252-991A-23386
US-09-252-991A-23386
US-09-253-991A-33196
US-09-489-039A-1106
US-09-489-039A-1106
US-09-252-991A-33196
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US-09-252-991A-2968
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US-09-134-000C-4497
US-09-134-000C-6657
US-09-146-661-2
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US-09-148-796A-2550
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                                                                                                      Sequence 12, Appl Sequence 18909, A Sequence 18909, A Sequence 27542, A Sequence 24977, A Sequence 24977, A Sequence 3386, A Sequence 31106, A Sequence 31106, A Sequence 31106, A Sequence 31065, A Sequence 2968, Ap Sequence 2968, Ap Sequence 20850, A Sequence 20850, Appli Sequence 2, Appli Sequence 
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US-09-252-991A-27456	US-09-579-174-14	US-09-107-858-14	US-08-758-621-14	US-09-579-174-2	US-09-107-858-2	US-08-758-621-2	US-09-461-436B-52	US-08-513-974B-360	US-08-513-974B-52	US-10-140-002-472	US-07-732-242C-7	US-09-247-155-163	US-09-579-174-23	US-09-579-174-22	US-09-107-858-23	US-09-107-858-22	US-09-621-976-5202
Sequence 27456, A	Sequence 14, Appl	Sequence 14, Appl	Sequence 14, Appl	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 52, Appl	Sequence 360, App	Sequence 52, Appl	Sequence 472, App	Sequence 7, Appli	Sequence 163, App	Sequence 23, Appl	Sequence 22, Appl	•	Sequence 22, Appl	Sequence 5202, Ap

ALIGNMENTS

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Sequence 13, Application US/09215212
Patent NO. 6372207
GENERAL INFORMATION:
APPLICANT: TEPPER, Mark
APPLICANT: CUNNINGHAM, Mark
APPLICANT: SHERRIS, David
APPLICANT: SHERRIS, David
APPLICANT: MCKENNA, Sean
TITLE OF INVENTION: IFNAR/IFN
TITLE OF INVENTION: IFNAR/IFN
FILE REFERENCE: TEPPERIA.SEQ
CURRENT APPLICATION NUMBER: US/09/215,212
CURRENT FILING DATE: 1998-12-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: TEPPER, Mark
APPLICANT: CUNNINGHAM, Mark
APPLICANT: EL TAYAR, David
APPLICANT: EL TAYAR, Nabil
APPLICANT: EL TAYAR, Nabil
APPLICANT: EL TAYAR, Nabil
APPLICANT: MCKENNA, Sean
TITLE OF INVENTION. IFNARZ/IFN COMPLEX
FILE REFERENCE: TEPPERIA.SEQ
CURRENT FILING DATE: 1998-12-18
CURRENT FILING DATE: 1998-12-18
PRIOR APPLICATION NUMBER: 60/068,295
PRIOR FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 12
LENGTH: 21
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
COTHER INFORMATION. Description of Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Description of Artificial Sequence: C terminal human ; OTHER INFORMATION: SIFNAR2 linked by linker to N terminal human IFNbeta US-09-215-212-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 12, Application US/09215212; Patent No. 6372207; GENERAL INFORMATION:
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US-09-215-212-13
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Best Local S
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Pred. No. 0.00023;
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US-09-252-991A-18909
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US-09-252-991A-18909
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; OTHER INFORMATION: Description of Artificial Sequence: C terminal human; OTHER INFORMATION: SIFNAR2 linked by linker to N terminal human IFNDeta
                                       PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 27542
LENGTH: 640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 18909
LENGTH: 360
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                           Sequence 27542, Application US/09252991A Patent No. 6551795
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GENERAL INFORMATION:
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LENGTH: 34
TYPE: PRI
TYPE: PRI
ORGANISM: Artificial Sequence
                                                                                                                                                                            APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196,136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
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CURRENT FILING DATE: 199-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
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PRIOR FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.0
ORGANISM: Pseudomonas aeruginosa
                           IYPE:
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Local Similarity 80.0%;
les 8; Conservation
                         PRT
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Pred. No. 42;
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Pred. No. 0.00038;
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GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOPTWARE: PATEENTIN Ver. 2.0
SEQ ID NO 46190
LENGTH: 321
TYPE: PRT
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Best Local S
Matches 7
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Patent No. 6703491
                                                           Best Local Similarity
Matches 6; Conserv
                                                                                            Query Match
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APPLICANT: MARC J. Rubenfield et al.
APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196:136
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Patent No. 6551795
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Best Local :
                                                                                                                                            OTHER INFORMATION: Xaa means any amino acid
                                                                                                                                                             ORGANISM: Drosophila melanogaster FEATURE:
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TYPE: PRT
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189 DFSAGLIIGGK 199
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                             1 EFGAGLVLGGQ 11
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7; Conservative
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8; Conserv
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2; Mismatches
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Pred. No. 77;
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Pred. No.
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RESULT 7 US-09-252-991A-24977

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US-09-252-991A-23386
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US-09-252-991A-24977
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GENERAL INFORMATION:
                                  GENERAL INFORMATION:
APPLICANT: Homburger et al.
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
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SEQ ID NO 24977
LENGTH: 903
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SEQ ID NO 23386
SOFTWARE: PatentIn Ver. SEQ ID NO 33609
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Patent No. 6551795
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERIGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
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TITLE OF INVENTION:
FILE REFERENCE: 107
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PRIOR APPLICATION NUMBER: US
PRIOR FILING DATE: 1998-07-27
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
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Local Similarity 64.3%;
les 9; Conservative
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UMBER: US 60/094,190
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NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
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77.8%;
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Pred. No. 2.5e+02;
1; Mismatches 1
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Pred. No. 4e+02;
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US-09-543-681A-7178
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                                                                                                                    ; ORGANISM: Klebsiella
US-09-489-039A-11069
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Best Local S
Matches 6
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SEQ ID NO 7178
LENGTH: 150
TYPE: PRT
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GENERAL INFORMATION:
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APPLICANT: Gary Bro
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Best Local
                                                            Matches
                                                                        Query Match
Best Local
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FILE REFERENCE: 2709,1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR PILING DATE: 1999-04-09
                                                                                                                                                                                                                                                                       TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 2709.2004001
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                                                                                                                                                   TYPE: PRT
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136 FGQGLGLGGEW 146
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26 FSAGLIIGG 34
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                                                       Similarity
7; Conserv
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                            FGAGLVLGGQF 12
                                                                                                                                                                                                                                                                                                                     Gary Breton et. al
                                                          Conservative
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                                                                                                                                 pneumoniae
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                                                                        Score 37; Pred. No.
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Pred. No.
                                                            Mismatches
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                                                                                      Length 443
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RESULT 12

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Sequence 2968, Application US/09540236
PATENT NO. 6673910
GENERAL INFORMATION:
APPLICANT: GATY L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO A
ITITLE OF INVENTION: FOR DIAGNOSTICS AND THER
FILE REFERENCE: 2709.2005-001
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: 1998-07-27
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US-09-540-236-2968
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NUMBER OF SEQ ID NOS:
SEQ ID NO 33065
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
TEMOTH. AE?
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NUMBER OF SEQ ID NOS: 3840
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Best Local :
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 574
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Pseudomonas aeruginosa
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72.7%;
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Pred. No.
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Pred. No.
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                                                             AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARAND THERAPEUTICS
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                                                                                                                                                APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING;
TITLE OF INVENTION: AEROGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AUGUSTA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE REFERENCE: 107196.136
CURRENT FILING DATE: 1990-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-07-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 20850
LENGTH: 239
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SEQ ID NO 29929
LENGTH: 213
TYPE: PRT
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US-09-252-991A-29929
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                                     Matches
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Best Local :
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Patent No. 6551795
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Best Local :
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APPLICANT: Marc J.
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LENGTH: 153
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
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                                                                                                                                       TYPE: PRT
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ORGANISM: M.catarrhalis
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                                                 Similarity
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7; Conserv
EFGAGLVLGG 10
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                                Conservative
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87.5%;
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                          Score 36; DB 4; Le
Pred. No. 2.4e+02;
2; Mismatches 2;
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Pred. No. 2.2e+02;
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Pred. No. 1
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                                                            Length 239;
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APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO AC:
TITLE OF INVENTION: ENTERCOCCCUS FAECALIS FO:
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: Patentin version 3.1
SEQ ID NO 4497
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US-09-252-991A-19484
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US-09-134-000C-4497
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US-09-252-991A-26774
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  Sequence 19484, Application US/09252991A
PATENT NO. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AN
TITLE OF INVENTION: AERUGINOSA FOR DIAC
                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS:
SEQ ID NO 26774
LENGTH: 278
TYPE: PRT
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APPLICANT: Marc J.
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
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b. 6551795
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MARC J. Rubenfield et al.

VENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS AVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              107196.136
Rubenfield et al.
NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53.7%;
87.5%;
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                                                                                                                                                                                                                                                                                                         53.7%;
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Pred. No. 2.5e
1; Mismatches
                                                                                                                                                                                                                                                                                                    Score 36; DB 4; 1
Pred. No. 2.9e+02;
                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .5e+02;
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                                                                                                                                                                                                                                                                                                                         Length 278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 242;
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                           TO PSEUDOMONAS
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GAGLVLGG 10

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FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 19884
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                                                              US-08-845-295A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-845-295A-2
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 Matches
                Query Match
Best Local
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Best Local Similarity
                                                                                                                                                                                                                    CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/017
FILING DATE: 17-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Cheryl J. Tubach
REGISTRATION NUMBER: 38,346
REFERENCE/DOCKET NUMBER: 7043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 37662-5075
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch
COMPUTER: IBM Compatib
                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: Windows SOFTWARE: Microsoft Word CURRENT APPLICATION DATA:
                                                                               MOLECULE TYPE:
                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
                                                                                       LENGTH: 584 amino
TYPE: Amino Acid
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/845,295A FILING DATE: 25-April-97
                                                                                                                                                                                        TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
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Similarity 7; Conserv
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                                                                                                                          584 amino acids
                                                                                                                                                                         423-229-1239
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   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              IBM Compatible
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                                                                                                                                                                                          423-229-6189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Enzymatic Process for the Manufacture Ascorbic Acid, 2-Keto-L-Gulonic Acid, 2-Keto-L-Gulonic Acid
                53.7%;
87.5%;
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77.8%;
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                Score 36;
Pred. No.
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Pred. No.
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5e+02;
                6.3e+02;
                               Length 584;
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RESULT 22
US-09-146-661-2
                                              GENERAL

APPLICANT: HUDDS,
TITLE OF INVENTION: Enzymatic
TITLE OF INVENTION: Ascorbic Acid, 2-Keto-,
TITLE OF INVENTION: Acid
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
CORRESSEE: Eastman Chemical Company
PORCESSEE: Pack 511
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CLASSIFICATION:
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/017,879; 08/845,295
FILING DATE: 17-May-96; 25-April-97
ATTORNEY/AGENT INFORMATION:
NAME: Cheryl J. Tubach
REGISTRATION NUMBER: 38,346
REGISTRATION NUMBER: 70432
TELECOMMUNICATION INFORMATION:
TELECHONE: 423-229-6189
TELEPHONE: 423-229-6189
                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-140-933-2
                                                                                                                                                                                                   Sequence 2, Application US/09146661
Patent No. 6136575
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                    Query Match 53.7%;
Best Local Similarity 87.5%;
Matches 7; Conservative
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US-09-140-933-2
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OPERATING SYSTEM: Windows 95
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/140,
FILLING DATE: 27-August-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
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LENGTH: 584 amino acids
TYPE: Amino Acid
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ZIP: 37662-5075
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk
COUNTRY: USA
ZIP: 37662-5075
                                   STREET: P.O. Box 511
CITY: Kingsport
STATE: Tennessee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCE:
CORRESPONDENCE ADDRESS:
Fastman Chemical Company
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: F.C.
CITY: Kingsport
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                        146 GGGLVLGG 153
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No. 6022719
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                                                                                                                                     Enzymatic Process for the Manufacture of Ascorbic Acid, 2-Keto-L-Gulonic Acid, and Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Enzymatic Process for the Manufacture of Ascorbic Acid, 2-Keto-L-Gulonic Acid, and Esters of 2-Keto-L-Gulonic Acid
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Pred. No. 6.3e+02;
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                                                                                                                                        Esters of 2-Keto-L-Gu
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REGISTRATION NUMBER: 38,346
REFERENCE/DOCKET NUMBER: 7043:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 423-229-6189
TELEPAX: 423-229-1239
INFORMATION FOR SEQ ID NO: 2:
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APPLICANT: Hubbs, John C.
TITLE OF INVENTION: Enzyma
TITLE OF INVENTION: Ascorb
TITLE OF INVENTION: 2-Keto
NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-146-661-2
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SEQUIENCE CHARACTERISTICS:
LENGTH: 584 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/09150515
Patent No. 6271006
                                                                                                                                                                                                                       ZIP: 37662-5075
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/150,
FILING DATE: 09-SEP-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 53.7%;
Best Local Similarity 87.5%;
Matches 7; Conservative
                                                                                                                   PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/017,879;

PILING DATE: 17-May-96; 25-April-97

ATTORNEY/AGENT INFORMATION:

NAME: Cheryl J. Tubach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOTTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/14
FILING DATE: 03-Septmeber-98
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Eastman Chemical Company
STREET: P.O. Box 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: 423-229-6189
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APPLICATION NUMBER: US 60/017,879; 08/845,295
FILING DATE: 17-May-96; 25-April-97
ATTORNEY/AGENT INFORMATION:
NAME: Cheryl J. Tubach
REGISTRATION NUMBER: 38,346
REFERENCE/DOCKET NUMBER: 70432
                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: P.O. BO
CITY: Kingsport
STATE: Tennesse
                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           146 GGGLVLGG 153
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SYSTEM: Windows 95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Enzymatic Process for the Manufacture of Ascorbic Acid, 2-Keto-L-Gulonic Acid, an 2-Keto-L-Gulonic Acid
                                                                                                                                                                                                                                                             US/09/150,515
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                                                                                                                                                                            08/845,295
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     맑
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Candida albicans US-09-248-796A-19668
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                                                                                                  ; ORGANISM: Enterococcus faecalis US-09-134-000C-6657
                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 25
                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Lynn Dougette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO.
TITLE OF INVENTION: ENTEROCOCCUS FAECALIS
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
CURRENT FILING DATE: 1998-08-13
                                                                                                                                                    NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6657
LENGTH: 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 19668
LENGTH: 809
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APPLICANT: Keith Weinstock et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                             Sequence 6657, Application US/09134000C Patent No. 6617156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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Patent No. 6747177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/055,778 PRIOR FILING DATE: 1997-08-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
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nes 7; Conserv
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2 FGAGLVLGG 10
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Pred. No.
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Pred. No. 6.3e+02;
                                                  Score 35; DB 4; Pred. No. 97;
                                  Mismatches
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                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Candida albicans
US-09-248-796A-21582
                                                                                                              US-09-621-976-5202
                                                                                                                                    RESULT 28
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                                                    Sequence 5202, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
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SOPTWARE: PatentIn version 3.1
SEQ ID NO 5500
LENGTH: 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 21582
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CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/134,000C CURRENT FILING DATE: 1998-08-13 PRIOR APPLICATION NUMBER: US 60/055,778 PRIOR FILING DATE: 1997-08-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 032796-032
APPLICANT: Dumas Milne Edwards, J.B. APPLICANT: Jobert, S. APPLICANT: Giordano, J.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 97
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Pred. No. 1.3e+02;
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Pred. No. 1
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Guerinot, Mary Lou et al.
TITLE OF INVENTION: METAL-REGULATED TRANSPORTERS AND USES THEREFOR
FILE REFERENCE: DCI-099CPDV
CURRENT APPLICATION NUMBER: US/09/107,858
CURRENT FILING DATE: 1998-06-30
EARLIER FILING DATE: 1998-06-30
EARLIER FILING DATE: 1996-11-27
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 22
LENGTH: 120
TYPE: PRT
COGANISM: Arabidopsis thaliana
US-09-107-858-22
                                                                                                                                                                                                                                      RESULT 30
US-09-107-858-23
; Sequence 23, Applicat:
; Patent No. 6163900
; GENERAL INFORMATION:
; ORGANISM: Arabidopsis thaliana US-09-107-858-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -23..-1
US-09-621-976-5202
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Best Local Similarity
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US-09-107-858-22
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                                               SOFTWARE: PatentIn Ver.
SEQ ID NO 23
LENGTH: 120
                                                                                                                                     APPLICANT: Guerinot, Mary Lou et al.
TITLE OF INVENTION: METAL-REGULATED TRANSPORTERS AND USES THEREFOR
FILE REFERENCE: DCI-099CCPU
CURRENT APPLICATION NUMBER: US/09/107,858
CURRENT FILING DATE: 1998-06-30
PARTITED ARRITANTION NUMBER: OG/7E0 CO1
                                                                                           EARLIER APPLICATION NUMBER: 08/758,621
EARLIER FILING DATE: 1996-11-27
NUMBER OF SEQ ID NOS: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET. 054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: PRECENT. pm
SEQ ID NO 5202
LENGTH: 107
TYPE: PRT
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                                    TYPE: PRT
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Pred. No. 1.7e+02;
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APPLICANT: Guerinot, Mary Lou et al.

APPLICANT: Guerinot, Mary Lou et al.

TITLE OF INVENTION: METAL-REGULATED TRANSPORTERS AND USES THEREFOR

FILE REFERENCE: DCI-099CDDV

CURRENT APPLICATION NUMBER: US/09/579,174

CURRENT FILING DATE: 2000-05-25

PRIOR APPLICATION NUMBER: 09/107,858

PRIOR APPLICATION NUMBER: 09/107,858

PRIOR FILING DATE: 1998-06-30

PRIOR FILING DATE: 1998-06-30

PRIOR APPLICATION NUMBER: 08/758,621

PRIOR APPLICATION NUMBER: 08/758,621

VERIOR FILING DATE: 1996-11-27

NUMBER OF SEQ ID NOS: 27

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 22

LENGTH: 120
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                                                                                                                             ORGANISM: Arabidopsis thaliana US-09-579-174-23
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US-09-579-174-23
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Best Local Similarity
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LENGTH: 120
TYPE: PRT
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Best Local Similarity
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US-09-579-174-22
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APPLICANT: Guerinot, Mary Lou et al.

TITLE OF INVENTION: METAL-REGULATED TRANSPORTERS AND USES THEREFOR

FILE REFERENCE: DCI-099CPDV

CURRENT APPLICATION NUMBER: US/09/579,174

CURRENT FILING DATE: 2000-05-25
                                                                                                 Query Match
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Patent No. 6590140
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                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 09/107,858
PRIOR FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: 08/758,621
PRIOR FILING DATE: 1996-11-27
NUMBER OF SEQ ID NOS: 27
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No. 6590140
                                                                                                                                                                                                                 SOFTWARE: PatentIn Ver. 2.0
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77 FSSGIILGTGFM 88
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                                                         Pred. No. 1.7e+02;
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Pred. No. 1.7e+02;
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Pred. No. 1.7e+02;
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RESULT 33 US-09-247-155-163

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US-07-732-242C-7
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APPLICANT: Duclert, Aymeric
APPLICANT: Bougueleret, Lydie
TITLE OF INVENTION: Complementary DNAs
FILE REFERENCE: GENSET.021A
CURRENT APPLICATION NUMBER: US/09/247,155A
CURRENT FILING DATE: 1999-02-09
EARLIER APPLICATION NUMBER: 60/074,121
EARLIER APPLICATION NUMBER: 60/074,121
EARLIER APPLICATION NUMBER: 60/081,563
EARLIER FILING DATE: 1998-04-13
EARLIER APPLICATION NUMBER: 60/096,116
EARLIER APPLICATION NUMBER: 60/096,116
EARLIER APPLICATION NUMBER: 60/096,116
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EARLIER FILING DATE: 1998-10-04
NUMBER OF SEQ ID NOS: 182
SOFTWARE: Patent.pm
SEQ ID NO 163
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Best Local
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NAME/KEY: SIGNAL
LOCATION: -34..-1
SOFTWARE: ASCII FORM
CURRENT APPLICATION DATA;
APPLICATION NUMBER: US/07/732,242C
FILING DATE: 19910718
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JPN 2-210178
FILING DATE: 10-AUG-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Uozumi, Takeshi; Masaki, Haruhiko;
APPLICANT: Hidaka, Makoto; Nakamura, Akira;
APPLICANT: Maeda, Michihisa; Yoneta, Yasuo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PEATURE:
NAME/KEY: UNSURE
LOCATION: 81,84,87,131,135,143,156
OTHER INFORMATION: Xaa'= any one of the twenty amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENERAL INFORMATION:
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TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                 COUNTRY: USA
ZIP: 10016-2088
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 0.72mb
COMPUTER: IBM PC compatible (NEC PC-9801 RX)
OPERATING SYSTEM: MS DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Maeda, Michihisa; Yoneta, Yasuo
TITLE OF INVENTION: Gene of Urease
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
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Local Similarity 54.5%;
les 6; Conservation
                                                                                                                                                                                                                                                                                                                                      STATE: New York
                                                                                                                                                                                                                                                                                                                                                              CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                     STREET:
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                                                                                                                                                                                                                                                                                                                                                                                     600 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                          Frishauf, Holtz, Goodman & Woodward, P.C
                                                                                                                                     US/07/732,242C
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Pred. No. 2.9e+02;
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RESULT 36
US-08-513-974B-52
; Sequence 52, Application US/08513974B
; Patent No. 6114139
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Best Local Similarity
Watches 6; Conserve
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                                                                                                                                                                                                              ; ORGANISM: Homo Sapien 
US-10-140-002-472
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SEQUENCE CHARACTERISTICS:
LENGTH: 222 amin
Type
                                                                                                                                                                                                                                        Prior Application removed - See Palm or File Wrapper NUMBER OF SEQ ID NOS: 550 SEQ ID NO 472 LENGTH: 229 TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maur
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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Best Local Similarity
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APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/140,002
                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: P3330R1C59
                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)972-1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER:
                                                                                           176 GEGFILGGVFV 186
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o. 6725730
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                                                                                                                       3 GAGLVLGGQFM 13
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Filvaroff, Ellen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Smith, Victoria
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87.5%;
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Pred. No. 3.4e+02;
2; Mismatches 3
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Pred. No. 3.3e+02;
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                                                                                                                                                                               Length 229;
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GENERAL INFORMATION:

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APPLICANT: HUSEY,
APPLICANT: HUSEY,
APPLICANT: FUJII, RYO
APPLICANT: Ohtaki, Tetsuya
APPLICANT: Ohtaki, Tetsuya
APPLICANT: PUKUSUMI, Shoji
APPLICANT: PUKUSUMI, Shoji
ITILE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
NUMBER OF SEQUENCES: 380
CORRESPONDENCE ADDRESS:
ADDRESSE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
US-08-513-974B-52
                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: JP 6-189274
FILING DATE: 11-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189273
FILING DATE: 11-AUG-1945
PRIOR APPLICATION NUMBER: JP 6-189272
APPLICATION NUMBER: JP 6-189272
                                                                                                                                        TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO:
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APPLICATION NUMBER: JP 6-326611
PILING DATE: 28-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-270017
PILING DATE: 02-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236357
FILING DATE: 30-SEP-1994
PRIOR DATE: 30-SEP-1994
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PRIOR APPLICATION DATA:
APPLICATION UNBER: 11
FILING DATE: 16-MAR-12
PRIOR APPLICATION DATA:
APPLICATION UNBER: 11
APPLICATION UNBER: 11
APPLICATION UNBER: 20-JAN-15
               TOPOLOGY: li
                                                                                                                       SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: JP 6
FILING DATE: 11-AUG-1994
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                            REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 45:
FELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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CURRENT APPLICATION DATA:
APPLICATION UNBER: US/08/513,974B
FILING DATE: 14-SEP-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/01599
FILING DATE: 10-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
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                                                       STRANDEDNESS
                                                                                               LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0
                                                                                 amino
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                                                                                                   252
                                                                      acid
                                                                                            amino acids
           peptide
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APPLICATION NUMBER: UP 7-00/1/,
FILING DATE: 20-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 6-326611
FILING DATE: 28-DEC-1994
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: UP 6-270017
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Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION UNMBER: US/08/APPLICATION: 536
PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION UMBER: PCT/JPETLING DATE: 10-AUG-1995
PRIOR APPLICATION DATA: APPLICATION UMBER: JP 7-0
PILING DATE: 19-AUG-1995
APPLICATION UMBER: JP 7-0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 11-AUG-1945
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6
                                                 FILING DATE: 11-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6
                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                      FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6:
FILING DATE: 30-SEP-1994
                                                                                                                                                                                                                          FILING DATE: 02-NOV-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
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TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
NUMBER OF SEQUENCES: 380
                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
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FILING DATE: 30-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: JP 7-057186
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STREET: 1
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Ohtaki, Tetsuya
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Ohgi, Kazuhiro
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                                                   JP 6-189273
JP 6-189272
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Pred. No. 3
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US-09-461-436B-52
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Patent No. 6538107
GENERAL INFORMATION:
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INFORMATION FOR SEQ INO: 360:
SEQUENCE CHARACTERISTICS:
LENGTH: 252 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Resnick, David S. REGISTRATION NUMBER: 34,235 REFERENCE/DOCKET NUMBER: 45' TELECOMMUNICATION INFORMATION: TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/461,436B
FILING DATE: 14-Dec-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ryo Ryjii
TITLE OF INVENTION: G Protein Coupled Receptor Protein,
Production, And Use Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS: Angell, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Shuji Hinuma
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                                                                                                                                                                                                            APPLICATION NUMBER: 08/513,974
FILING DATE: 14-SEP-1995
APPLICATION NUMBER: PCT/JP95/01599
FILING DATE: 10-AUG-1995
APPLICATION NUMBER: 7-093989
FILING DATE: 19-APR-1995
APPLICATION NUMBER: 7-057186
FILING DATE: 16-MAR-1995
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APPLICATION NUMBER: 6-236357
FILING DATE: 30-SEP-1994
APPLICATION NUMBER: 6-236356
FILING DATE: 30-SEP-1994
APPLICATION NUMBER: 6-189274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: MA
                                                                                                                                    FILING DATE: 20-JAN-1995
APPLICATION NUMBER: 6-326611
FILING DATE: 28-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: BOSTON
                                                                                                APPLICATION NUMBER: 6-270 FILING DATE: 02-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/09461436B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yasuaki Ito
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Pred. No. 3.7e+02;
                                                                                                                    6-270017
                                                                                                                                                                                              7-007177
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Best Local Similarity
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Query Match
Best Local Similarity
6; Conserve
                                                                              ; MOLECULE TYPE: protein US-08-758-621-2
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US-08-758-621-2
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; SEQUENCE DESCRIPTION: SEQ ID NO: 52:
US-09-461-436B-52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application Patent No. 5846821
GENERAL INFORMATION:
                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/018,578
FILING DATE: 29-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Silveri, Jean M.
REGISTRATION NUMBER: 39,030
REFERENCE/DOCKET NUMBER: DCI-099
                                                                                                                                                                 TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELBFAX: 617-439-4170
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/758,621
FILING DATE:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Guerinot, Mary Lou, and Eide, David J.
TITLE OF INVENTION: Metal-Regulated Transporters and Uses Therefor
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
                                                                                                                               TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Boston
                                                                                                                TOPOLOGY:
                                                                                                                                               LENGTH:
                                                                                                                                                                                                                     TELEPHONE:
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NAME: CONLIN, DAVID G.
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RÉFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-439-4444
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FILING DATE: 11-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: <Unknown>
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              Conservative
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                            50.0%;
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                                                                                                                                                                                                                                                         DCI-099CP
              Score 35; DB 2;
Pred. No. 5.1e+02;
3; Mismatches 3
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                                              Length 339;
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Title:
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Match
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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Gapop 10.0 ,
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2861
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     Copyright
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     GenCore version 5.1.6 (c) 1993 - 2004 Compugen
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157.08-716-317-7

15.08-792-01.98-9

15.08-988-819-9

15.08-98-89-7

15.08-99-30-537-45

15.08-99-30-371A-27

15.09-230-371A-27

15.09-239-856-6

15.09-439-856-6

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US-08-795-4738-5
US-09-439-856-5
5171840-2
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US-09-213-942-15
5171840-7
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US-09-313-942-24
5171840-6
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5171840-5
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Sequence 8, Appli
Sequence 5, Appli
Sequence 5, Appli
Patent No. 5480796
Sequence 15, Appl
Patent No. 5480796
Sequence 26, Appl
Sequence 27, Appl
Sequence 24, Appl
Sequence 16, Appl
Patent No. 5471840
Patent No. 5480796
Sequence 16, Appli
Sequence 1, Appli
Patent No. 5171840
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TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND
TITLE OF INVENTION: AND USING
FILE REFERENCE: REG 203-A
CURRENT APPLICATION NUMBER: US/09/313,942
CURRENT FILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: 09/313,942
PRIOR PILING DATE: 1999-05-19
PRIOR PILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: 60/101,858
PRIOR APPLICATION NUMBER: 60/101,858
UNMBER OF SEQ ID NOS: 32
SOFTWARE: PASTSEQ for Windows Version 3.0
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; LENGTH: 592
; TYPE: PRT
; ORGANISM: HO
US-09-313-942-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 8, Application Patent No. 6472179 GENERAL INFORMATION:
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US-09-313-942-8
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ALIGNMENTS

US/09313942

AND METHODS

OF MAKING

Similarity CFRKSPLSNVVCEWGPRSTPSLTTKAVLLVRKFQNSPAEDFQEPCQYSQESQKFSCQLAV PEGDSSFYIVSMCVASSVGSKFSKTQTFQGCGIIQPDPPANITVTAVARNPRWLSVTWQD VLRKPAAGSHPSRWAGMGRRLLLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPEEPQLS GEWSEWSPEAMGTPWTESRSPPAENEVSTPMQALTTNKDDDNILFRDSANATSLPVEFMP PHSWNSSFYRLRFELRYRAERSKTFTTWMVKDLQHHCVIHDAWSGLRHVVQLRAQEEFGQ VLRKPAAGSHPSRWAGMGRRLLLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPEEPQLS GEWSEWSPEAMGTPWTESRSPPAENEVSTPMQALTTNKDDDNILFRDSANATSLPVQ---PHSWNSSFYRLRFELRYRAERSKTFTTWMVKDLQHHCVIHDAWSGLRHVVQLRAQEEFGQ PEGDSSFYIVSMCVASSVGSKFSKTQTFQGCGILQPDPPANITVTAVARNPRWLSVTWQD Conservative 67.1%; Score 1921; DB 4 77.1%; Pred. No. 8e-151; tive 22; Mismatches 4 4 44; Indels 46; Length 592; Gaps 180 120 300 240 180 120 60 60 300 240

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TYPE: amino acids
TYPE: amino acid
TYPE: unknown
US-08-795-473B-5
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Best Local Similarity 96.5%;
Matches 360; Conservative
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INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 468 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-D
SOFTWARE: MS-DOS EDITOR
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795
FILING DATE: 11-FEB-1997
CLASSIFICATION:
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APPLICANT: Nahot, Orit
APPLICANT: Blum, Herbert E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Davidson, Clifford M.
REGISTRATION NUMBER: 32,728
REFERENCE/DOCKET NUMBER: 963.1007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)-997-1028
TELEPHONE: (212)-997-1028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: A Pharmaceutical Composition for Treating TITLE OF INVENTION: Hepatitis B Virus (HBV) Infection NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
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PEGDSSFYIVSMCVASSVGSKFSKTQTFQGCGILQPDPPANITVTAVARNPRWLSVTWQD
                                                            CFRKSPLSNVVCEWGPRSTPSLTTKAVLLVRKFQNSPAEDFQEPCQYSQESQKFSCQLAV
                                                                                           CFRKSPLSNVVCEWGPRSTPSLTTKAVLLVRKFQNSPAEDFQEPCQYSQESQKFSCQLAV
                                                                                                                                    VLRKPAAGSHPSRWAGMGRRLLLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPEEPQLS
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1140 Avenue of the Americas
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Matches
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APPLICATION NUMBER: 08/795,473

APPLICATION NUMBER: 10-FEB-1997

APTONNEY/ACENT INFORMATION:

NAME: Davidson, Clifford M.

REGISTRATION NUMBER: 32,728

REFERENCE/DOCKET NUMBER: 963.1007

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)-997-1028
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INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Nahot, Urit APPLICANT: Blum, Herbert E. TITLE OF INVENTION: A Pharmaceutical Composition for Treating TITLE OF INVENTION: Hepatitis B Virus (HBV) Infection OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS-DOS EDITOR
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 468 amino acid
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COUNTRY:
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STATE: New York
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                                                                                                                                                                                                                                                                                    TYPE: amino acid
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CFRKSPLSNVVCEWGPRSTPSLTTKAVLLVRKFQNSPAEDFQEPCQYSQESQKFSCQLAV
                                                                     VLRKPAAGSHPSRWAGWGRRLLLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPPEEPQLS 120
                                                                                                                                    MLAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHW
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                                                    VLRKPAAGSHPSRWAGMGRRLLLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPEEPQLS
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1140 Avenue of the Americas
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Nahot, Orit
Blum, Herbert E.
                                                                                                                                                                                                                                                                                                    468 amino acids
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                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                  67.0%;
96.5%;
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                                                                                                                                                                               Score 1918; DB 4
Pred. No. 1e-150;
1; Mismatches
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PATERIE NO. 5171840

APPLICANT: KISHIMOTO, TADAMITSU

TITLE OF INVENTION: RECEPTOR PROTEIN FOR APPLICATION PROTEIN FOR SEQUENCES: 11

CURRENT APPLICATION NUMBER: US/07/298,694

FILING DATE: 19-JAN-1989

SEQ ID NO:2:
RESULT 5
5480796-2
;Patent NO. 5480796
; APPLICANT: KISHIMOTO, TADAMITSU
; TITLE OF INVENTION: ANTIBODIES AGAINST THE RECEPTOR PROTEIN
; FOR HUMAN B CELL STIMULATORY FACTOR-2
; NUMBER OF SEQUENCES: 8
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Best Local Similarity 96.5
Matches 360; Conservative
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96.5%;
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                                                                Query Match
Best Local S
Matches 355
                                                                                                                                                                                                                                                  Sequence 15, Application US/09313942
Patent No. 6472179
GENERAL INFORMATION:
APPLICANT: REGENERON PHARMACEUTICALS, INC.
APPLICANT: REGENERON PHARMACEUTICALS, INC.
TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING TITLE OF INVENTION: AND USING
FILE REFERENCE: REG 203-A
CURRENT APPLICATION NUMBER: US/09/313,942
CURRENT FILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: 09/313,942
PRIOR APPLICATION NUMBER: 60/101,858
PRIOR FILING DATE: 1998-09-25
PRIOR FILING DATE: 1998-09-25
PRIOR FILING DATE: 1998-09-25
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 15
LENGTH: 360
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Best Local Similarity 96.5%;
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FILING DATE: 02-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 298,694
FILING DATE: 19-JAN-1989
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                                                                 Local Similarity
nes 355; Conserv
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MVAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTCPGVBPEDNATVHW
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Pred. No. 3.1e-150;
2; Mismatches 0;
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5480796-7
; PATENT NO. 5480796
; APPLICANT: KISHIMOTO, TADAMITSU
; TITLE OF INVENTION: ANTIBODIES AGAINST
; FOR HUMAN B CELL STIMULATORY FACTOR-2
; NUMBER OF SEQUENCES: 8
; CURRENT APPLICATION DATA:
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TITLE OF INVENTION: RECEPTOR
STIMULATORY FACTOR-2
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/
FILING DATE: 19-JAN-1989
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ECEPTOR PROTEIN FOR HUMAN
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; SEQ ID NO 26
; LENGTH: 1158
; TYPE: PRT
; ORGANISM: Homo 9
US-09-313-942-26
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CURRENT APPLICATION NUMBER: US/09/313,94
CURRENT FILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: 09/313,942
PRIOR FILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: 60/101,858
PRIOR FILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 3.
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Best Local Similarity
Matches 344; Conserv
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Patent No. 6472179
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APPLICANT: REGENERON PHARMACEUTICALS,
TITLE OF INVENTION: RECEPTOR BASED AN
TITLE OF INVENTION: AND USING
                                                                                                           Matches
                                                                                                                                     Query Match
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FILING DATE: 02-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 298,694
FILING DATE: 19-JAN-1989
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                                                                                                        Local Similarity nes 331; Conserv
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                                                                                                           Score 1788; DB 4;
Pred. No. 2.4e-139;
2; Mismatches 1;
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: REGENERON PHARMACEUTICALS, INC.

TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND

TITLE OF INVENTION: AND USING

FILE REFERENCE: REG 203-A

CURRENT APPLICATION NUMBER: US/09/313,942

CURRENT FILING DATE: 1999-05-19

PRIOR APPLICATION NUMBER: 09/313,942

PRIOR APPLICATION NUMBER: 09/313,942

PRIOR APPLICATION NUMBER: 60/101,858

PRIOR APPLICATION NUMBER: 60/101,858

PRIOR FILING DATE: 1999-05-19

PRIOR APPLICATION NUMBER: 09-25

NUMBER OF SEQ ID NOS: 32

SOFTWARE: FASTSEQ for Windows Version 3.0

SEQ ID NO 24

LENGTH: 1168

TYPE: PRT

ORGANISM: Homo sapiens
RESULT 11
5171840-6
;Patent No. 5171840
; APPLICANT: KISHIMOTO, TADAMITSU
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Best Local Similarity
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Pred. No. 6.2e-139;
1; Mismatches 0;
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;Patent No. 5480796
; APPLICANT: KISHIMOTO, TADAMITSU
; TITLE OF INVENTION: ANTIBODIES AGAINST
; FOR HUMAN B CELL STIMULATORY FACTOR-2
NUMBER OF SEQUENCES: 8
; CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/907,650
FILLING DATE: 02-UUL-1992
; PRIOR APPLICATION DATA:
APPLICATION NUMBER: 298,694
; APPLICATION DATE: 19-JAN-1989
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NUMBER OF SEQUENCES: 11

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/298,694

FILING DATE: 19-JAN-1989
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Best Local Similarity
Matches 322; Conserv
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Best Local Similarity
Matches 322; Conserv
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                                                                                              VLRKPAAGSHPSRWAGMGRRLLLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPEEPQLS
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                                CFRKSPLSNVVCEWGPRSTPSLTTKAVLLVRKFQNSPAEDFQEPCQYSQESQKFSCQLAV
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GENERAL INFORMATION:

APPLICANT: REGEDERON PHARMACEUTICALS, INC.

TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, ANI

TITLE OF INVENTION: AND USING

FILE REFERENCE: REG 203-A

CURRENT APPLICATION NUMBER: US/09/313,942

CURRENT FILING DATE: 1999-05-19

PRIOR APPLICATION NUMBER: 09/313,942

PRIOR APPLICATION NUMBER: 09/313,942

PRIOR PILING DATE: 1999-05-19

PRIOR APPLICATION NUMBER: 60/101,858

PRIOR FILING DATE: 1999-05-19

PRIOR FILING DATE: 1998-09-25

NUMBER OF SEQ ID NOS: 32

SOFTWARE: FASTSEQ for Windows Version 3.0

SEQ ID NO 16
                                                                                                                                   RESULT 14
5171840-5
                          PATENT NO. 5171840

APPLICANT: KISHIMOTO, TADAMITSU
TITLE OF INVENTION: RECEPTOR PROTEIN
STIMULATORY FACTOR-2
NUMBER OF SEQUENCES: 11
CURRENT APPLICATION DATA:
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US-09-313-942-16
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                 APPLICATION NUMBER:
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Local Similarity 99.7%;
nes 312; Conservation
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Pred. No. 1.8e-131;
1; Mismatches 0; Indels
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                                                                                 HUMAN
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5480796-5
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APPLICANT: KISHIMOTO, TADAMITSU
ITILE OF INVENTION: ANTIBODIES AGAINST THE RECEPTOR PROTEIN
FOR HUMAN B CELL STIMULATORY FACTOR-2
NUMBER OF SEQUENCES: 8
CURRENT APPLICATION DATA:
CURRENT APPLICATION NUMBER: US/07/907,650
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 298,694
FILING DATE: 19-JAN-1989
SEQ ID NO:5:
LENGTH: 386
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                                                                                                                                                                                                                                                              Query Match 48.5
Best Local Similarity 73.6
Matches 276; Conservative
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Matches 276; Conserv
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                          179
                                                                                121 CFRKSPLSNVVCEWGPRSTP--SLTTKAVLLVRKFQNSPAEDFQEPCQYSQESQKFSCQL
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AVPEGDSSFYIVSMCVASSVGSKFSKTQTFQGCGILQPDPPANITVTAVARNPRWLSVTW
                                                   CFRKSPLSNVVC--GPRSTPEWSLTTKAVLLVRKFQNSPAEDFQEPCQYSQESQKFSCQL
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                                                                                                                                                                                                                                                       48.5%; Score 1389; DB 6; Length 386; 73.6%; Pred. No. 5.9e-107; tive 1; Mismatches 4; Indels 9
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Pred. No. 5.9e-107;
1; Mismatches 4;
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RESULT 17
5171840-11
; Patent No. 5171840
; APPLICANT: KISHIMOTO, TADAMITSU
; TITLE OF INCENTION: RECEPTOR PROTEIN FOR HUMAN B CELL
; STIMULATORY FACTOR-2
; NUMBER OF SEQUENCES: 11
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/298,694
; FILING DATE: 19-JAN-1989
; SEQ ID NO:11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 16
US-09-043-785-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 40.3%; Score 1153; DB 3; Best Local Similarity 100.0%; Pred. No. 9.2e-88; Matches 210; Conservative 0; Mismatches 0;
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SEQ ID NO 1
LENGTH: 210
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ORGANISM: Human
-09-043-785-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: SYNTHETIC PEPTIDES THAT INHIBIT IL-6 ACTIVITY
FILE REFERENCE: Chebath=1
CURRENT APPLICATION NUMBER: US/09/043,785
CURRENT FILING DATE: 1998-09-02
EARLIER APPLICATION NUMBER: PCT/IL96/00119
EARLIER FILING DATE: 1996-09-26
EARLIER FILING DATE: 1996-09-26
EARLIER APPLICATION NUMBER: 115,453
EARLIER FILING DATE: 1995-09-26
EARLIER FILING DATE: 1995-09-26
EARLIER APPLICATION NUMBER: 118,097
EARLIER FILING DATE: 1996-05-01
NUMBER: OF SEQ ID NOS: 4
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APPLICANT: HALIMI, Hubert
APPLICANT: REVEL, Michel
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                                                                                                                                                                                                                                                                                                                                                                RAQEEFGQGEWSEWSPEAMGTPWTESRSPP 322
                                                                                                                                                                                                                                                                                                                                                                                                                               WLSVTWQDPHSWNSSFYRLRFELRYRAERSKTFTTWMVKDLQHHCVIHDAWSGLRHVVQL
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                                                                                                                                                                                                                                                                                                                                     RAQEEFGQGEWSEWSPEAMGTPWTESRSPP 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KFSCQLAVPEGDSSFYIVSMCVASSVGSKFSKTQTFQGCGILQPDPPANITVTAVARNPR
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US-08-716-317-7
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Patent No.
                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/716,317
FILING DATE: 02-OCT-1996
CLASSIFICATION LOTA:
APPLICATION NUMBER: PCT/JP96/00198
FILING DATE: 01-PEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 17167/1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 17167/1995
FILING DATE: 03-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 59-924-0 PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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                                                                                                                      TELEPHONE: 703-413-300
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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APPLICANT:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: SECRETION SIGNAL GENE AND EXPRESSION TITLE OF INVENTION: VECTOR CONTAINING IT NUMBER OF SEQUENCES: 35
                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 703-413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS
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                                                TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, ADDRESSEE: P.C. STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 22202
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                                                                                              185 amino acids
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                                                  single
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Pred. No. 6e-71;
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                                                                                            US-08-792-019B-9
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                                                                                                                                                                                                                                                  CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: COOK, ROBERT R.
REGISTRATION NUMBER: 31,60
REFERENCE/DOCKET NUMBER: A
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 9, Application US/08792019B Patent No. 5741772
GENERAL INFORMATION:
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                                          Matches 187;
                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: CHANG, MITTITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/792,019B
FILING DATE: 03-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: AMGEN INC.
STREET: 1840 DEHAVILLAND
CITY: THOUSAND OAKS
                                                                                                                                   FEATURE:
                                                                                                                                                                                    MOLECULE TYPE:
                                                                                                                                              NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: sin
                                                                                                        LOCATION:
                                                                                                                     NAME/KEY:
                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U
                                                                                                                                                                                                                                       ENGTH:
354 LPVEF-MPVPPGEDSKDVAAPHRQPLTSSERIDKQIRYILDGISALRKETCNKSNMCESS
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                                                                                                                                                                                                                                       212 amino acids
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                                          Conservative
                                                                                                        Region
                                                                                                                                              Protein
1..182
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                                     Score 938.5; DB 1;
Pred. No. 5.9e-70;
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Pred. No.
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; LOCATION: US-08-988-819-9
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                                                                                                                                 Query Match
Best Local Similarity
Matches 187; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 31,6
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                      FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/792,019
FILING DATE: 03-FEB-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy |
COMPUTER: IBM PC com
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ADDRESSEE: AMGEN INC.
STREET: ONE AMGEN CENTER DRIVE
                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/988,819 FILING DATE: 12-DEC-1997
                                                                                                                                                                                                                                                                                           NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: THOUSAND OAKS
                                                                                                                                                                                                                                                                           LOCATION:
                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: COOK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         413 KEALAENNLNLPKMAEKDGCFQSGFNEETCLVKIITGLLEFEVYLEYLQNRFESSEEQAR
                                                                                        354 LPVEF-MPVPPGEDSKDVAAPHRQPLTSSERIDKQIRYILDGISALRKETCNKSNMCESS
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              KEALAENNINI PKWAEKDGCFQSGFNEETCLVKI ITGLLEFEVYLEYLQNRFESSEEQAR
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                                                               LPAAFPAPVPPGEDSKDVAAPHRQPLTSSERIDKQIRYILDGISALRKETCNKSNMCESS
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Pred. No. 5.9e-70;
0; Mismatches 3
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                                                                                                                                                                                                     Matches
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APPLICANT: CHANG, MING-SHI
APPLICANT: ELLIOTT, GARY S.
APPLICANT: SARMIENTO, ULLA
APPLICANT: SARMIENTO, ULLA
APPLICANT: SENALDI, GIORGIO
TITLE OF INVENTION: THE NEUROTROPHIC FACTOR NNT-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: COOK, ROBERT R.
REGISTRATION NUMBER: 31,602
REFERENCE/DOCKET NUMBER: A-4
INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 03-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: COOK, ROBERT R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,534
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ADDRESSEE: AMGEN INC.
STREET: ONE AMGEN CENTER
                                                                                                                                                                                                                                                                                                                       FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
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LOCATION:
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                                                              82 KEALAENNINIPRIAEKOGCFQSGFNEETCLVKIITGLLEFEVYLEYLQNRFESSEEQAR 141
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 AVQMSTKVLIQFLQKKAKNLDAITTPDPTTNASLLTKLQAQNQWLQDMTTHLILRSFKEF 201
                    AVQMSTKVLIQFLQKKAKNLDAITTPDPTTNASLLTKLQAQNQWLQDMTTHLILRSFKEF
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97.9%;
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Pred. No. 5.9e-70;
0; Mismatches 3;
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RESULT 23
US-08-795-473B-6
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US-08-097-869-7
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                       Matches 187; Conservative
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APPLICATION NUMBER: US 07/753,178
FILING DATE: 30-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: MUTASHIGE, Kate H.
REGISTRATION NUMBER: 29,959
REGISTRATION NUMBER: 24455-2000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-813-5600
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APPLICANT: Todaro
APPLICANT: Rose,
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/097,869
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CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy disk
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CLASSIFICATION:
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97.9%;
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Pred. No. 5.9e-70;
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GENERAL INFORMATION:
APPLICANT: Galun, Eithan
APPLICANT: Whent, Orit
APPLICANT: Blum, Herbert E.
APPLICANT: Blum, Herbert E.
TITLE OF INVENTION: Hepatitis B Virus (HBV) Infection
TITLE OF INVENTION: Hepatitis B Virus (HBV) Infection
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                                                                                                                                                                                                                                                                                                                            Sequence 45, Application US/09230637 Patent No. 6264958
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Best Local Similarity
                          APPLICANT: Hayward, Gary
APPLICANT: Nicholas, John
APPLICANT: Hardwick, J. Marie
APPLICANT: Reitz, Marvie
APPLICANT: Reitz, Marvie
TITLE OF INVENTION: No. 6264958el Genes of Kaposi's
TITLE OF INVENTION: Associated Herpesvirus
FILE REFERENCE: 1107.78372
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
CURRENT APPLICATION NUMBER: US/09/230,637
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NAME: DAVIDSON, Clifford M.
REGISTRATION NUMBER: 32,728
REFERENCE/DOCKET NUMBER: 96:
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US/08/795,473B
FILING DATE: 11-FEB-1997
CLASSIFICATION:
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STREET: 12.
STREET
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SOFTWARE: MS-DOS EDITOR
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TOPOLOGY: unknow
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Pred. No. 5.9e-70;
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; LENGTH: 212
; TYPE: PRT
; ORGANISM: Human
US-09-230-371A-27
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PRIOR APPLICATION NUMBER: 60/025
PRIOR FILING DATE: 1996-07-25
PRIOR APPLICATION NUMBER: PCT US
PRIOR FILING DATE: 1997-07-24
PRIOR FILING DATE: 1997-07-24
NUMBER OF SEQ ID NOS: 62
SOFTWARE: FastSEQ for Windows Value of the control of the contr
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US-09-230-371A-27
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Best Local Similarity 97.9
Matches 187; Conservative
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SOFTWARE: PatentIn V
SEQ ID NO 27
LENGTH: 212
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CURRENT FILING DATE: 1999-11-17
PRIOR APPLICATION NUMBER: PCT/US97/13346
PRIOR FILING DATE: 1997-07-22
NUMBER OF SEC. TO THE RESERVE OF SEC.
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APPLICANT: Russo, James J
APPLICANT: Edelman, Isidore S
APPLICANT: Moore, Patrick S
TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS
TITLE OF INVENTION: USES THEREOF
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Pred. No. 5.9e-70;
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Pred. No. 5.9e-70;
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APPLICATION NUMBER: 08/795,473
PILING DATE: 11-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Davidson, Clifford M.
REGISTRATION NUMBER: 32,728
REFERENCE/DOCKET NUMBER: 963.1007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)-997-1028
TELEPHONE: (212)-997-1037
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APPLICANT:
APPLICANT:
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MEDIUM TYPE: 3.5 inch disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS-DOS EDITOR
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/439,856 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: New York
STATE: New York
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LOSSLRALROM 212
                              LOSSLRALROM 543
                                                                   AVQMSTKVLIQFLQKKAKNLDAITTPDPTTNASLLTKLQAQNQWLQDMTTHLILRSFKEF
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Blum, Herbert E.
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                                                                                                                                                                                                                                                                                                                                                                  unknown
                                                                                                                                                                                                                                                                                                                                                                                                   212 amino acids
                                                                                                                                                                                                                                                                                           32.8%;
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                                                                                                                                                                                                                                                                           Score 938.5; DB 4; Length 212;
Pred. No. 5.9e-70;
0; Mismatches 3; Indels 1
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RESULT

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NUMBER OF SEQ ID NOS: 41

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 13

LENGTH: 212

TYPE: PRT

ORGANISM: Homo sapiens
US-09-462-941-13
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                                                                                                                                                                                               SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                     INTERFERON-BETA2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No.
                                                                                                  Matches 187;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 13, Appli
Patent No. 6608183
                                                                                                                  Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Cox III, George N
APPLICANT: Bolder Biotechnology, Inc.
TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
FILE REFERENCE: 4152-1-PUS
CURRENT APPLICATION NUMBER: US/09/462,941
CURRENT FILING DATE: 2000-01-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/052,516
PRIOR FILING DATE: 1997-07-14
                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/
FILING DATE: 15-MAY-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 9
                                                                                                                                                                                 LENGTH: 212
                                                                                                                                                                                                                                     APPLICATION
                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                   APPLICATION NUMBER: 860,883 FILING DATE: 08-MAY-1986
                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 449,447 FILING DATE: 12-DEC-1989
                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 208,925 FILING DATE: 20-NOV-1980
                                                                                                                                                                                                                  FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           473 AVQMSTKVLIQFLQKKAKNLDAITTPDPTTNASLLTKLQAQNQWLQDMTTHLILRSFKEF 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           354 LPVEF-MPVPPGEDSKDVAAPHRQPLTSSERIDKQIRYILDGISALRKETCNKSNMCESS
                                                     354 LPVEF-MPVPPGEDSKDVAAPHRQPLTSSERIDKQIRYILDGISALRKETCNKSNMCESS
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413 KEALAENNILNIPKMAEKDGCFQSGFNEETCIVKIITGLIEFEVYLEYIQNRFESSEEQAR 472
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                                22 LPAAFPAPVPPGEDSKDVAAPHRQPLTSSERIDKQIRYILDGISALRKETCNKSNMCESS
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                                                                                                    Conservative
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N: PRODUCTION OF RECOMBINANT HUMAN
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Pred. No. 5.9e-70;
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US-08-469-318-145
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/44
FILING DATE:
FILING DATE:
INFORMATION FOR SEQ ID NO: 14
SEQUENCE CHARACTERISTICS:
LENGTH: 317 amino acids
GTD ANTERNACION ACID
                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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TITLE OF INVENTION: Protein
NUMBER OF SEQUENCES: 196
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EF
APPLICATION NUMBER: US/08/469,318
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GENERAL INFORMATION:
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                                                                                                           457 LEYLQNRFESSEEQARAVQMSTKVL1QFLQKKAKNLDAITTPDPTTNASLLTKLQAQNQW
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o. 6022535
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                                                             LQDMTTHLILRSFKEFLQSSLRALRQM 543
                                                                                      LEYLQNRFESSEEQARAVQMSTKVLIQFLQKKAKNLDAITTPDPTTNASLLTKLQAQNQW
                                                                                                                                                   ALRKETCNKSNMCESSKEALAENNLNLPKMAEKDGCFQSGFNEETCLVKIITGLLEFEVY
                                                                                                                                                                      ALRKETCNKSNMCESSKEALAENNLNLPKMAEKDGCFQSGFNEETCLVKIITGLLEFEVY
                                                                                                                                                                                                                                                                                                 HVVQLRAQEEFGQGEWSEWS------PEAMGTPWT-ESRSPPAENEVSTPMQALTT 336
                                                                                                                                                                                                                                                                                                                               DPNNLNSEDMDILMERNLRTPNLLAFVR-AVKHLENASGIEAILRNLQPCLPSATAAPSR
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                                                                                                                                                                                                            -ŚGGGSNM----APVPPGEDSKDVAAPHRQPLTSSERIDKQIRYILDGIS
                                                                                                                                                                                                                                                                                                                                                                                          32.7%; Score 935; DB 3; Length 317; 63.0%; Pred. No. 2.1e-69; ative 17; Mismatches 48; Indels
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                                                                                                                                                                                                                                                                    -GDWQEFREKLTFYLVTLEQAQEQQYVIEGRISPGGG----- 125
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Best Local
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INFORMATION FOR SEQ ID NO: 145:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/192
FILING DATE: 14-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bennett, Dennis A.
REGISTRATION NUMBER: 34,547
REFERSNCE/DOCKET NUMBER: C-27
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)737-5986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 60680

COMPUTER ERADABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0,

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/468,609,

FILING DATE: 06-UUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 145, Application US/08468609A
Patent No. 6030812
GENERAL IMPORMATION:
APPLICANT: Abrams, Mark A.
                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
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APPLICANT:
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APPLICANT:
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APPLICANT: Thomas, John W.
APPLICANT: Thomas, John W.
TITLE OP INVENTION: Fusion Proteins Comprising Multiply Mutated Inteleukin-3 (IL-
NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: P. O. BO:
CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 317 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
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                                457
                                                                                                                                                                                                                                                                                                          240 DPHSWNSSFYRLRFELRYRAERSKTFTTWMVKDLOH------HCVIHDAWSGLR 287
                                                                                                                                                                                                              83
                                                                                                                                                                                                                                                                                                                                                        206;
                                                                                                                                                                                                                                                                                     24
                                                                                                                                                                                                                                                                                                                                               h 32.7%; Score 935; DB 3; Length 317;
Similarity 63.0%; Pred. No. 2.1e-69;
06; Conservative 17; Mismatches 48; Indels
LEYLONRFESSEEQARAVOMSTKVL10FLQKKAKNLDAITTPDPTTNASLLTKLQAQNOW 516
                                                       ALRKETCNKSNMCESSKEALAENNLNLPKMAEKDGCFQSGFNEETCLVKIITGLLEFEVY
                                                                            ALRKETCNKSNMCESSKEALAENNLNLPKWAEKDGCFQSGFNEETCLVKIITGLLEFEVY 456
                                                                                                                                                     NKDDDNILFRDSANATSLFVEFMFVFFGEDSKDVAAPHRQFLTSSERIDKQIRYILDGIS
                                                                                                                                                                                                                                   HVVQLRAQEEFGQGEWSEWS------PEAMGTPWT-ESRSPPAENEVSTPMQALTT 336
                                                                                                                                                                                                                                                                        DPNNLNSEDMDILMERNLRTFNLLAFVR-AVKHLENASGIEAILRNLQPCLPSATAAPSR
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Easton, Alan M.
Klein, Barbara K.
McKearn, John P.
Olins, Peter O.
Paik, Kumnan
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                                                                                                                                                                                                                                                                                                                                                                                                                                              protein
                                                                                                                            SGGGSNM----APVPPGEDSKDVAAPHRQPLTSSERIDKQIRYILDGIS
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RESULT 31
US-08-446-872A-145
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                                                                                                                         Matches 206;
                                                                                                                                          Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                 TELEFAX: (314)737-6972
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/446,872;
FILING DATE: 06-UUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/192,325
FILING DATE: 14-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Fusion Protein NUMBER OF SEQUENCES: 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (314)737-6986
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: P. O. CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 34,547
REFERENCE/DOCKET NUMBER: C-2790/1
                                                                                                                                                                                                                                                                                                                                                                               NAME: Bennett, Dennis
REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                   STRANDEDNESS
                                                                                                                                                                                                                                                                LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Corporate Patent Dept.
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                            288 HVVQLRAQEEFGQGEWSEWS------PEAMGTPWT-ESRSPPAENEVSTPMQALTT 336
                                                                                          240 DPHSWNSSFYRLRFELRYRAERSKTFTTWMVKDLQH------HCVIHDAWSGLR 287
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                                                                                                                                                                                                                                                     amino acid
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                                                              DPNNLNSEDMDILMERNLRTPNLLAFVR-AVKHLENASGIEAILRNLQPCLPSATAAPSR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Illinois
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Paik, Kumnan
                                                                                                                                                                                                                                                                    317 amino acids
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                                                                                                                           Conservative
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Klein, Barbara K.
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Caparon, Maire H.
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                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dennis A. Bennett, G.D. Searle & Co.,
                                                                                                                                                                                                     protein
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                                                                                                                                          32.7%;
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GDWQEFREKLTFYLVTLEQAQEQQYVIEGRISPGGG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US/08/446,872A
                                                                                                                                                                                                                                                                                                     145:
                                                                                                                         17;
                                                                                                                                          Score 935; DB 3; Pred. No. 2.1e-69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sarah
                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Version #1.25
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                                                                                                                           48;
                                                                                                                                                         Length 317;
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; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 145:
US-08-762-227A-145
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US-08-762-227A-145
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GENERAL INFORMATION:
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                                                                                                                                            INFORMATION FOR SEQ ID NO: 145:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Easton, Alan M.
Klein, Barbara K.
McKearn, John P.
Olins, Peter O.
Paik, Kumman
Thomas, John W.
TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis
                                                                                                                                                                                                                   NAME: Bennett, Dennis A. REGISTRATION NUMBER: 34,5 REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION.
                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 08/446,872
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/192,325
FILING DATE: 14-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 197 CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/762,227A FILING DATE: 09-Dec-1996 CLASSIFICATION: <Unknown>
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Corporate Patent Dept.
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                                                                                 STRANDEDNESS:
                                                                                                    TYPE: amino acid
                                                                                                                                                                                  TELEPHONE: (708)470-6501
TELEPAX: (708)470-6881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 60680
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                                                            TOPOLOGY: linear
                                                                                                                           LENGTH:
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Maire H.
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Easton, Alan M.
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                                                                                                                       317 amino acids
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                                                                                   <Unknown>
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PCT-US95-01185-145
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                                                                                                                                                                                                       Matches 206;
                                                                                                                                                                                                                                           Query Match
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Best Local Similarity
Matches 206; Conserv
                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/192325
FILING DATE: 14-FEB-1994
INFORMATION FOR SEQ ID NO: 145:
SEQUENCE CHARACTERISTICS:
LENGTH: 317 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0
                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 0
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                              TOPOLOGY:
337 NKDDDNILFRDSANATSLPVEFMPVPPGEDSKDVAAPHRQPLTSSERIDKQIRYILDGIS
                                                                                       288 HVVQLRAQEEFGQGEWSEWS------PEAMGTPWT-ESRSPPAENEVSTPMQALTT 336
                                                                                                                                                            240 DPHSWNSSFYRLRFELRYRAERSKTFTTWMVKDLQH------HCVIHDAWSGLR 287
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                                                                                                                             DPNNLNSEDMDILMERNLRTPNLLAFVR-AVKHLENASGIEAILRNLQPCLPSATAAPSR
                                                    HPIIIKA-----GDWQEFREKLTFYLVTLEQAQEQQYVIEGRISPGGG-------
                                                                                                                                                                                                                                                                                                                                                 amino acid
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                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                             protein
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                                                                                                                                                                                                                    32.7%;
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                                                                                                                                                                                                    17;
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                                                                                                                                                                                                    Score 935; DB 5; Length 317; Pred. No. 2.1e-69; 7; Mismatches 48; Indels
                                                                                                                                                                                                  56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56;
                                                                                                                                                                                                  Gaps
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; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 184 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-567-047-2
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                                                                                Matches
                                                                                                                       Query Match
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Patent No. 5789552
Patent No. 5789552 5789555
                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/387,924
FILING DATE: 23-FB-1995
APPLICATION NUMBER: IT RM93A000409
FILING DATE: 23-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGET L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: SAVINO=1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: METHOD FOR SELECTING SUPERAGONISTS,
TITLE OF INVENTION: ANTAGONISTS AND SUPERANTAGONISTS FOR HORMONES HAVING
TITLE OF INVENTION: GP 130 AS PART OF THEIR RECEPTOR COMPLEX
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: SAVINO, ROCCO
APPLICANT: LAHM, Armin
APPLICANT: CILIBERTO, Gennaro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 419 Sevent
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Palane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 04-DEC CLASSIFICATION: 530
                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                TELEPHONE: 202-620
                   360 PVPPGEDSKDVAAPHRQPLTSSERIDKQIRYILDGISALRKETCNKSNMCESSKEALAEN 419
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PVPPGEDSKDVAAPHRQPLTSSERIDKQIRYILDGISALRKETCNKSNMCESSKEALAEN
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                                                                            32.6%; Score 934; DB 1; 1 larity 100.0%; Pred. No. 1.1e-69; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                  202-628-5197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US/08/567,047
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                                                                                                                  Length 184;
                                                                              Indels
                                                                            Gaps
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RESULT 35
US-08-567-048-2
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Best Local S
Matches 184
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APPLICANT: SAVINO,
APPLICANT: LAHM, A
APPLICANT: CILIBER
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                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/567,048
FILING DATE: 04-DEC-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/387,924
FILING DATE: 23-FEB-1995
APPLICATION NUMBER: IT RM93A000409
FILING DATE: 23-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGEY L.
REFERENCE/DOCKET NUMBER: 25,618
REFERENCE/DOCKET NUMBER: SAVINO=1
TELEFONE: 202-628-5197
TELEFAX: 202-628-5197
TELEFAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: LAHM, Armin
APPLICANT: CILIBERTO, Gennaro
TITLE OF INVENTION: METHOD FOR SELECTING SUPERAGONISTS,
TITLE OF INVENTION: ANTAGONISTS AND SUPERANTAGONISTS FOR HORN
TITLE OF INVENTION: GP 130 AS PART OF THEIR RECEPTOR COMPLEX
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NOTED
                                                                                                                                                                                                                                                                                                                        TELEX: 248633
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET:
                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           540
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                420 NLNLPKMAEKDGCFQSGFNEETCLVKIITGLLEFEVYLEYLQNRFESSEEQARAVQMSTK
                                                                                                360 PVPPGEDSKDVAAPHRQPLTSSERIDKQIRYILDGISALRKETCNKSNMCESSKEALAEN
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                                                                                                                                                    184;
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                                                                                                                                                                                                                                                                                  amino acids
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NLNLPKMAEKDGCFQSGFNEETCLVKIITGLLEFEVYLEYLQNRFESSEEQARAVQMSTK 120
                                                                      PVPPGEDSKDVAAPHRQPLTSSERIDKQIRYILDGISALRKETCNKSNMCESSKEALAEN
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419 Seventh Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                32.6%; So illarity 100.0%; E Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IT RM93A000409
                                                                                                                                                Score 934; DB 2; ; Pred. No. 1.1e-69; 0; Mismatches 0;
                                                                                                                                                                                      Length 184
                                                                                                                                                    Indels
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                                                                                                                                                    0
                                                                                                                                                Gaps
                                  479
                                                                        60
                                                                                                              419
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PATENT NO. 5186931

PATENT NO. 5186931

APPLICANT: Kishimoto, Tadamitsu;Hirano, Toshio;Akiyama, Yukio;
Okano, Akira;Matsui, Hiroshi;Takahara, Yoshiyuki

TITLE OF INVENTION: COMPOSITION AND METHOD FOR SUPPORTING BONE
MARROW TRANSPLANTATION

NUMBER OF SEQUENCES: 2

CURRENT APPLICATION NUMBER: US/07/366,866
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US-07-632-070B-1
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                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/07632070B Patent No. 5264209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                        GENERAL INFORMATION:

APPLICANT: Mikayama, Toshihumi
APPLICANT: Kadoya, Toshihiko
APPLICANT: APPLICANT: Kakitani, Makoto
APPLICANT: APPLICANT: Inoue, Hideo
TITLE OF INVENTION: Modified hIL-6
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/07,
FILING DATE: 15-UUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 81,746
FILING DATE: 05-AUG-1987
                                      COMPUTER READABLE FORM: MEDIUM TYPE: Diskette,
                                                                                                                                  STREET: 2
CITY: Chi
COMPUTER: IBM COMPATIBLE OPERATING SYSTEM: MS-DOS
                                                                                              COUNTRY: United States of America
                                                                                                                                                                      ADDRESSEE: Marshall, O'Toole, Gerstein, ADDRESSEE: Murray & Bicknell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             360 PVPPGEDSKDVAAPHRQPLTSSERIDKQIRYILDGISALRKETCNKSNMCESSKEALAEN 419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           420 NLNLPKWAEKDGCFQSGFNEETCLVKIITGLLEFEVYLEYLQNRFESSEEQARAVQMSTK 479
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                                                                            60603
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                                                                                                                Illinois
                                                                                                                                                      20 South Clark Street,
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                                                                                                                                    1 cago
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                                      5.25 inch, 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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                                                                                                                                                        Suite 2100
                                        Kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 184;
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US-07-918-181A-2
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                 COMPUTER REALABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/918,181A
FILING DATE: 23-JUL-1992
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sheets, Eric J.
REGISTRATION MIMBER: 30,326
REFERENCE/DOCKET NUMBER: FOW-2
TELECOMMUNICATION INFORMATION:
TELEPAN: 212-645-1405
TELEPAN: 212-645-2054
TELEPAN: 212-645-2054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-07-632-070B-1
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GENERAL INFORMATION:
APPLICANT: Fowlkes, Dana M.
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FILING DATE: 13 FEB 1990
APPLICATION NUMBER: JP 2-22
FILING DATE: 22 AUG 90
APPLICATION NUMBER: JP 2-25
FILING DATE: 21 SEPT 1990
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 185
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Matches
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          TELEFAX: 212-645-2054
                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: C-Terminal IL-6 Muteins
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: ImClone Systems Incorporated
STREET: 180 Varick Street
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                   STREET: 10.
STREET: 10.
STREET: New York
New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
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100.0%; Pr
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; MOLECULE TYPE: protein US-08-231-575-2
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Query Match 32.6%; Score 934; DB 1; Best Local Similarity 100.0%; Pred. No. 1.1e-69; Matches 184; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/231,575
FILING DATE: 22-ARR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 07/918,181
FILING DATE: 23-UTL-1992
ATTORNEY, AGENT INFORMATION:
NAME: Sheets, Eric J.
REGISTRATION NUMBER: 30,326
REGERENCE/DOCKET NUMBER: FOW-2
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO: 2:
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Best Local Similarity
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APPLICANT: Fowlker
                                                                                                                                                   SEQUENCE CHARACTERISTICS
LENGTH: 185 amino aci
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TITLE OF INVENTION: C-Terminal IL-6 Muteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                      TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
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STATE: New York
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TYPE: amino acid
TOPOLOGY: linear
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amino acid
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180 Varick Street
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Length 185;

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US-08-246-427A-5
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INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 185 AWINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY. ILVERE
                                                                                                                                                  Query Match 32.6%; Score 934; DB 1; Length 185; Best Local Similarity 100.0%; Pred. No. 1.1e-69; Matches 184; Conservative 0; Mismatches 0; Indels
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PS/2

OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/246,427A
FILING DATE: Submitted herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/246,427
FILING DATE: MAY 19, 1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-
TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
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TITLE OF INVENTION: Interleukin-6 Splice Variant
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CARCULI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: ROSELAND
STATE: NEW JERSEY
                                                                       182 LRQM 185
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NLNLPKWAEKDGCFQSGFNEETCLVKIITGLLEFEVYLEYLQNRFESSEEQARAVQMSTK 121
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1910	1910	1910	1910	1912	1913	1915	1915.5	1917	1918	1918	1918	1918	1918	1918	1918	1921	1921	1921	2149.5	2512.5	2646	2663.5	2769.5	2861	Score
66.8	66.8		66.8	•	66.9		67.0	67.0	67.0	67.0	67.0	67.0	67.0	67.0	67.0	67.1	67.1	67.1	75.1	87.8	2	93.1	96.8	100.0	Query Match I
468	360	360	360	477	357	468	468	690	468	468	468	468	468	468	468	592	592	592	419	500	525	515	570	543	Length D
_	7	ω	N	w	σ	N	w	w	7	σ	ഗ	v	4.	Ν	۲	7	w	N	N	N	ผ	w	0	N	DB
AAP90525	ABW02172	AAY92199	AAW70804	AAY92197	ABP72699	AAR98364	AAY92196	AAY92195	ADC07187	ABP72697	ABB78191	AAE28593	AAB36655	AAR37215	AAP90284	ABW02165	AAY92185	AAW70797	AAY30938	AAW36847	AAW36846	AAB15404	ABP72702	AAY03164	ID
Aap90525 B cell st	Abw02172 Human IL-	Aay92199 Soluble h	Aaw70804 Amino aci	Aay92197 Human IL-	Ţ	Aar98364 Interleuk	Human	Aay92195 Human IL-	Adc07187 Human IL-	Abp72697 Human int	Abb78191 Amino aci	Aae28593 Interleuk	Aab36655 Human IL-		Aap90284 Sequence	Abw02165 Human IL-	Aay92185 Human IL-	Aaw70797 Human int	Aay30938 Human IL-	Aaw36847 Human fus	Aaw36846 Human fus	Aab15404 IL-6R/IL-	Abp72702 Human int	Aay03164 Chimeric	Description

4	44	43	42	41	40	39	38	37	36	35	34	33	32	<u>υ</u>	30	29	28	27	26
1683	1683	1683	1715	1742	1748	1748	1748	1754	1757	1759	1763	1783	1783	1788	1788	1852	1858	1900	1907
58.8	58.8	58.8	59.9	60.9	61.1	61.1	61.1	61.3	61.4	61.5	61.6	62.3	62.3	62.5	62.5	64.7	64.9	66.4	66.7
315	315	315	323	325	325	325	325	325	325	1042	325	1168	1168	1158	1158	344	345	468	364
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ABW02173	AAY92200	AAW70805	AAP90527	AAO23017	AAO23015	AAB15390	AAB15389	AA023018	AAO23016	AAR70122	AAO23014	ABW02177	AAY92204	ABW02178	AAY92205	AAP90528	AAY55071	AAW71371	ABP72698
Abw02173	Aay92200	Aaw70805	Aap90527	Aao23017	Aao23015	Aab15390	Aab15389	Aao23018	Aao23016	Aar70122	Aao23014	Abw02177	Aay92204	Abw02178	Aay92205	Aap90528	Aay55071	Aaw71371	App72698
Human IL-	Soluble h	Amino aci	B cell st	Human in	Human int	Bovine in	Human int	Human int	Human int	IL8-R ty		Human cyt	Fusion po	Human cyt	Fusion po	B cell st	SR345 pro	Human int	Soluble

ALIGNMENTS

Chimeric sIL-6R/IL-6 protein. 11-JUN-1999 AAY03164; AAY03164 standard; protein; (first entry) 543 A

Soluble interleukin-6 receptor; interleukin-6; sIL-6; IL-6; sIL-6/IL-6; chimeric protein; fusion protein; cell growth inhibitor; melanoma cell; highly malignant cancer cell; in vivo engraftment; mammalian cancer; human haematopoietic cell; bone marrow transplantation; mammalian cancer; hepatotoxic agent protection; haematopoiesis; liver disorder; neurological disorder.

Synthetic.

WO9902552-A2

21-JAN-1999

09-JUL-1998; 98WO-IL000321.

10-JUL-1997; 30-DEC-1997; 97IL-00121284. 97IL-00122818.

(YEDA) YEDA RES & DEV CO LTD.

Revel M, Chebath J, Lapidot T, Kollet

Ö

WPI; 1999-120776/10.

New glycosylated soluble IL-6 receptor/IL-6 conjugates - used treating cancers, bone marrow transplantation, increasing haem or treating liver or neurological disorders. used for e.g. haematopoiesis

Claim 6; Fig 3; 77pp; English.

RESULT 1
AAY03164
ID AAY03164
AAY 03464
AAY 03 This sequence represents the chimeric glycosylated soluble interleukin-6 receptor (sII-6R)-interleukin-6 (II-6) protein (sII-6R/II-6) of the invention. It comprises a fusion protein product between all of the naturally occurring form of sIL-6R and all of the naturally occurring form of II-6, the sIL-6/II-6 and analogues being glycosylated in a similar fashion to the glycosylation of naturally occurring sII-6R and III-6. The sIL-6/II-6 and analogues are capable of inhibiting the growth of highly malignant cancer cells, e.g. melanoma cells, eliciting the in vivo

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RESULT 2
ABP72702
ID ABP7
XX ABP7
XX ABP7
XX ABP7
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XX Huma
XX Huma
XX Huma
XX Homc
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OS Chim
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Best Local :
 Synthetic. Chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   engraftment of human haematopoietic cells in bone marrow transplantation and protecting liver from hepatotoxic agents. They can be used for the preparation of a medicament for treating mammalian cancers by way of inhibition of cancer cells, for enhancement of bone marrow transplantation by way of eliciting engraftment of human haematopoietic cells in bone marrow transplantation, for increasing haematopoiesis, for treating liver or neurological disorders, or in other applications in which IL-6 or sIL-6R are used
                                                                         Human; interleukin-6; receptor; DS-sIL-6R; antibacterial; virucide;
anti-HIV; antirheumatic; antiarthritic; antiinflammatory;
                                                                                                                                                    11-JUN-2003
                                                                                                                                                                                  ABP72702
                                                                                                                                                                                                             ABP72702 standard;
                             Homo sapiens
                                                        immunosuppressive; gene therapy.
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                                                                                                                    interleukin-6-receptor isoform DS-sIL-6R fusion protein
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                                                                                                                                                                                                                                                                                                                                               LIQFLQKKAKNLDAITTPDPTTNASLLTKLQAQNQWLQDMTTHLILRSFKEFLQSSLRAL
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                                                                                                                                                                                                                                                                                                                                                                                                                            LNLPKMAEKDGCFQSGFNEETCLVKIITGLLEFEVYLEYLQNRFESSEEQARAVQMSTKV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VLRKPAAGSHPSRWAGMGRRLLLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPEEPQLS
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                                                                                                                                                                                                                                                                                       ROM
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Pred. No. 4
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4.2e-183;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is the protein sequence of a novel fusion protein CC comprising a soluble form of the human interleukin-6 receptor, denoted DS CC -sIL-6R (see also ABP72698), joined via a peptide linker to a human IL-6 cm of comprising a soluble form of the human interleukin-6 receptor, denoted DS CC administration of this fusion protein results in the increased expression of one or more of MIP-lalpha, MIP-lbeta, RANTES or IP-10. High levels of CC MIP-lalpha, MIP-lbeta, MIP-beta, RANTES or IP-10. High levels of CC and effectively suppress HIV entry. The fusion protein can be used in the treatment of any disease in which the infectious agent binds to CCR5, cespecially M-trophic strains of HIV. The invention also provides a complete acid molecule encoding the fusion protein, an expression vector, a host cell, and a method of producing the fusion protein in the host cell. The fusion protein, nucleic acid or vector can be used in the colling construction of a medicament for the prophylaxis or treatment of an infectious disease (especially AIDS caused by a M-trophic strain of HIV, cor bacterial peritonitis), an inflammatory disorder or an immunological cor bacterial peritonitis), an immune response (claimed)
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New fusion protein having a functional II-6 and DS-sIL-6R molecule, useful for the manufacture of a medicament for the prophylaxis or treatment of an infectious disease, and an inflammatory or immunolous treatment of an infectious disease, and an inflammatory or immunolous treatment of an infectious disease, and an inflammatory or immunolous treatment of an infectious disease, and an inflammatory or immunolous treatment of an infectious disease, and an inflammatory or immunolous treatment of an infectious disease, and an inflammatory or immunolous treatment of an infectious disease, and an inflammatory or immunolous treatment of an infectious disease, and an inflammatory or immunolous treatment for the prophylaxis or the prop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 570 AA;
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VPEGDSSFYIVSMCVASSVGSKFSKTQTFQGCGILQPDPPANITVTAVARNPRWLSVTWQ
                                                                                                                       CFRKSPLSNVVCEWGPRSTPSLTTKAVLLVRKFQNSPAE-DFQEPCQYSQESQKFSCQLA
                                                                                                                                                                                                                                              VLRKPAAGSHPSRWAGMGRRLLLLRS VQLHDSGNYSCYRAGRPAGTVHLLVDVPPEEPQLS
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                                                                                                                                                                                                        VLRKPAAGSHPSRWAGMGRRLLLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPEEPQLS
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                                                                                 CFRKSPLSNVVCEWGPRSTPSLTTKAVLLVRKFQNSPAEDDFQEPCQYSQESQ-FSCQLA
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365. .376
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 2769.5;
Pred. No. 6e-1
0; Mismatches
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180

VPEGDSSFYIVSMCVASSVGSK-SKTQTFQGCGILQPDPPANITVTAVARNPRWLSVTWQ

238 239 179 179

120 120 Gaps

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Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fusion protein; hur drug; myeloid stem
The invention relates to the production of a fusion protein comprising the human interleukin 6 receptor (IL-6R) fused to the human IL-6 protein in a Pichia pastoris yeast cell. This sequence represents the IL-6R/IL-6 fusion protein. The coding sequence for this protein is cloned into an expression vector for introduction into P. pastoris. The IL-6R protein is used as a drug for amplifying myeloid stem cells and increasing platelets
                                                                                                                                                      Yeast of Pichia Pastoris genus transformed by expression vector containing gene encoding fused protein of interleukin-6 receptor (IL-6R) protein for amplifying myeloid stem cells and increasing platelets.
                                                                                                                                                                                                                               N-PSDB; AAA70763.
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                                                                                                                       Example 1; Page 8-10; 11pp; Japanese
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protein interaction; therapeutic; antagonist.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RLLLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPEEPQLSCFRKSPLSNVVCEWGPRST
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(first en
                                                                                                                                                                                                                                                                                         polypeptide H-IL-6 with 18 amino acid linker
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/label=
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/note= "Links together COOH-terminus
NH2-terminus of IL-6"
                                                                                                                                            Location/Qualifiers
                                                                         /note=
                                                                                                                                                                                                                                                                                                                                                                                                                   protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence represents the fusion polypeptide H-II-6 which contains a la amino acid linker which joins the carboxy terminus of human interleukin-6 (II-6). Such conjugates could be used to modulate interactions between proteins, particularly to overcome interrupted interactions caused by an incomplete interleukin-6 (II-6) receptor. The constructs derived from II-6 and its receptor, can also be used for exvivo expansion of human stem cells, and as a therapeutic II-6 receptor antagonist. (Updated on 25-MAR-2003 to correct PI field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conjugate of two peptide(s) with mutual affinity connected by a linker used to modulate interactions between proteins, e.g. for ex vivo expansion of human stem cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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DB; AAT97848.
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LIQFLQKKAKNLDAITTPDPTTNASLLTKLQAQNQWLQDMTTHLILRSFKEFLQSSLRAL
                   LIQFLQKKAKNLDAITTPDPTTNASLLTKLQAQNQWLQDMTTHLILRSFKEFLQSSLRAL
                                                                                                                               VPPGEDSKDVAAPHRQPLTSSERIDKQIRYILDGISALRKETCNKSNMCESSKEALAENN
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                                                        LNLPKWAEKDGCFQSGFNEETCLVKIITGLLEFEVYLEYLQNRFESSEEQARAVQMSTKV
                                                                              LNLPKMAEKDGCFQSGFNEETCLVKIITGLLEFEVYLEYLQNRFESSEEQARAVQMSTKV
                                                                                                             VPPGEDSKDVAAPHRQPLTSSERIDKQIRYILDGISALRKETCNKSNMCESSKEALAENN
                                                                                                                                                                     GEWSEWSPEAMGTPWTESRSPPARGGGGS------
                                                                                                                                                                                              GEWSEWSPEAMGTPWTEGRSPPAENEVSTPMQALTTNKDDDNILFRDSANATSLPVEFMP
                                                                                                                                                                                                                         PHSWNSSFYRLRFELRYRAERSKTFTTWMVKDLQHHCVIHDAWSGLRHVVQLRAQEEFGQ
                                                                                                                                                                                                                                            PHSWNSSFYRLRFELRYRAERSKTFTTWWVKDLQHHCVIHDAWSGLRHVVQLRAQEEFGQ
                                                                                                                                                                                                                                                                                                  PEGDSSFYIVSMCVASSVGSKFSKTQTFQGCGILQPDPPANITVTAVARNPRWLSVTWQD
                                                                                                                                                                                                                                                                                                                                                                CFRKSPLSNVVCEWGPRSTPSLITKAVLLVRKFQNSPAEDFQEPCQYSQESQKFSCQLAV
                                                                                                                                                                                                                                                                                                                                                                                              VLRKPAAGSHPSRWAGMGRRLLLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPEEPQLS
                                                                                                                                                                                                                                                                                                                                                                                                              VLRKPAAGSHPSRWAGMGRRLLLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPEEPQLS
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                                                                                                                                                                                                                                                                                  PEGDSSFYIVSMCVASSVGSKFSKTQTFQGCGILQPDPPANITVTAVARNPRWLSVTWQD
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93.7%;
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Indels

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                             Query Match
Best Local
                                                                                                                                                                           This sequence represents the fusion polypeptide H-IL-6 which contains a 13 amino acid linker which joins the carboxy terminus of human interleukin-6 receptor (IL-6R) with the amino terminus of human interleukin-6 (IL-6). Such conjugates could be used to modulate interactions between proteins, particularly to overcome interrupted interactions caused by an incomplete interleukin-6 (IL-6) receptor. The constructs derived from IL-6 and its receptor, can also be used for exvivo expansion of human stem cells, and as a therapeutic IL-6 receptor analysomist. (Updated on 25-MAR-2003 to correct PR field.) (Updated on 2
                                                                                                           Sequence
                                                                                                                                                           antagonist.
MAR-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conjugate of two peptide(s) with mutual affinity connected by a linker - used to modulate interactions between proteins, e.g. for ex vivo expansion of human stem cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rosejohn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Interleukin-6; IL-6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human fusion polypeptide H-IL-6 with 13 amino acid linker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-MAR-2003
25-MAR-1998
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DB; AAT97849.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of human stem
                                                                                                                                                           (Updated on 25-MAR-2003 correct PI field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                            Fig 2; 19pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Links together
NH2-terminus of IL-6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label=
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90.1%;
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Score 2512.5; DB 2; Pred. No. 8.3e-160; 1; Mismatches 10;
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New interleukin-6 receptor-interleukin-6 fused protein for growth of bone marrow stem cells and platelets.
                                                                                                                                                                                                                                                                                                                   JP11196867-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IL-6; interleukin-6; receptor; human; fusion protein;
stem cell; platelet; reduced antigenicity.
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                                                                    N-PSDB; AAZ09202.
                                                                                      WPI; 1999-496648/42
                                                                                                                                                                             09-JAN-1998;
                                                                                                                                                                                                                          09-JAN-1998;
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1. .420
/note= "No start co
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                                                                                                                                                          Synthetic.
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This invention describes a novel gene which encodes a fusion protein of interleukin-6 (II-6) receptor and bound with a gene sequence encoding for II-6 at the downstream of II-6 receptor gene. The gene and its encoding protein has applications for the growth of bone marrow stem cells and platelets. Transmission of a signal of II-6 to target cells for stimulation with reduced antigenicity is possible. This sequence represents the II-6 receptor/II-6 fusion protein described in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Page 5-8; 8pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                 EEFGQGEWSEWSPEAMGTPWTESRSPPAENEVSTPMQALTTNKDDDNILFRDSANATSLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VTWQDPHSWNSSFYRLRFELRYRAERSKTFTTWMVKDLQHHCVIHDAWSGLRHVVQLRAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CQLAVPEGDSSFYIVSMCVASSVGSKFSKTQTFQGCGILQPDPPANITVTAVARNPRWLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EPQLSCFRKSPLSNVVCEWGPRSTPSLTTKAVLLVRKFQNSPAEDFQEPCQYSQESQKFS
                                MSTKVLIQFLQKKAKNLDAITTPDPTTNASLLTKLQAQNQWLQDMTTHLILRSFKEFLQS
                                                                                                               LAENNINIPKMAEKDGCFQSGFNEETCIVKIITGILDFEVYLEYIQNRFESSEEQARAVQ
                                                                                                                                            LAENNLNL PKWAEKDGCFQSGFNEETCLVKI I TGLLEFEVYLEYLQNR FESSEEQARAVQ
                                                                                                                                                                                                                              ---APVPPGEDSKDVAAPHRQPLTSSERIDKQIRYILDGISALRKETCNKSNMCESSKEA
                                                                                                                                                                                                                                                                  VEFMPVPPGEDSKDVAAPHRQPLTSSERIDKQIRYILDGISALRKETCNKSNMCESSKEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CQLAVPEGDSSFYIVSMCVASSVGSKFSKTQTFQGCGILQPDPPANITVTAVARNPRWLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EPOLSCFRKSPLSNVVCEWGPRSTPSLTTKAVLLVRKFQNSPAEDFQEPCQYSQESQKFS
MSTKVLIQFLQKKPKNLDAITTPDPTTNASLLTKLQAQNQWLQDMTTHLILRSFKDFLQS
                                                                                                                                                                                                                                                                                                                                              EEFGQGEWSEWSPEAMGTPWTESRSPPAENEVSTPMQALTTNKDDDNILSSELV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                       VTWQDPHSWNSSFYRLRFELRYRAERSKTFTTWMVKDLQHHCVIHDAWSGLRHVVQLRAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 2149.5; DB 2
Pred. No. 1.4e-135;
3; Mismatches 6;
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gpl30; cytokine antagonist; interleukin; gamma-interferon; peptid
              /note= "human IL-R-alpha"
1. .19
/note= "signal peptide"
                                                                 Location/Qualifiers
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Matches 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents the amino acid sequence of human interleukin (II)-6R-alpha-Fc. The protein is used in the course of the invention. The specification describes cytokine antagonists component only the extracellular domain of the specificity-determining component of the cytokine receptor and the extracellular domain of a signal-transducing component of the cytokine receptor. The cytokine is an interleukin (II-1, II-2, II-3, II-4, II-5 or II-15), granulocyte macrophage colony-stimulating factor (CM-CSF), gamma-interferon or transforming growth factor-beta (TGF-beta). The antagonist is capable of transforming growth factor-beta (TGF-beta). The antagonist is capable of binding the cytokine to form a nonfunctional complex. The compounds have therapeutic activity as cytokine antagonists and can also be used in assays for identifying novel agonists and antagonists of cytokines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yancopoulos GD,
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                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                            MVAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHW
                                                                                                                                                                                                                                                                                                                                                        MLAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHW
                                                                                                                                                                                                                                                                                         VLRKPAAGSHPSRWAGWGRRLLLRSVOLHDSGNYSCYRAGRPAGTVHLLVDVPPEEPQLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                 592 AA
                                                                                                                                                                                                                                CFRKSPLSNVVCEWGPRSTPSLTTKAVLLVRKFQNSPAEDFQEPCQYSQESQKFSCQLAV
                                                                                                                                                                                                                                                                      VLRKPAAGSHPSRWAGMGRRLLLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPEEPQLS
                                                        GEWSEWSPEAMGTPWTESRSPPAENEVSTPMQALTTNKDDDNILFRDSANATSLPVEFMP
                                                                                             PHSWNSSFYRLRFELRYRAERSKTFTTWMVKDLQHHCVIHDAWSGLRHVVQLRAQEEFGQ
                                                                                                                                                    PEGDSSFYIVSMCVASSVGSKFSKTQTFQGCGILQPDPPANITVTAVARNPRWLSVTWQD
                                                                                                                                                                       PEGDSSFYIVSMCVASSVGSKFSKTQTFQGCGILQPDPPANITVTAVARNPRWLSVTWQD
                                                                                                                                                                                                             CFRKSPLSNVVCEWGPRSTPSLTTKAVLLVRKFQNSPAEDFQEPCQYSQESQKFSCQLAV
      VPPGEDSKDVAAPHRQPLTSSERIDKQIRYILDGISALRKETÇNKSNMCE--SSKEALAE
                                    GEWSEWSPEAMGTPWTESRSPPAENEVSTPMQALTTNKDDDNILFRDSANATSLPVQ---
                                                                                                             Conservative
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371. .:
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                                                                                                                                                                                                                                                                                                                                                                                                      67.1%; Score 1921; DB 2; 77.1%; Pred. No. 4.2e-120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "changed to accomodate a Kozak sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             comprising extracellular domains of specificity-transducing components of cytokine receptor.
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The invention concerns production of antagonists to any cytokine that utilizes an alpha specificity determining component, which when combined with the cytokine, binds to a first beta signal transducing component to form a non-functional intermediate which then binds to a second beta signal transducing component causing beta-receptor dimerization, the soluble alpha specificity determining component of the receptor (gR-alpha) and the extracellular domain of the first beta signal transducing component of the cytokine receptor (beta-1) are combined to form heterodimers (gR-alpha) should be the cytokine and the cytokine by the combined to the cytokine by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disulfide-bond
                                                                                                                                                                                                                                                                                                           Isolated nucleic acid molecule for treating cytokine-related disorders encodes a fusion polypeptide capable of binding a
                                                                                                                                                                                                                                                                                                                                                                                                                                   Stahl N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-APR-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 377
           Cytokine; cytokine-related disease; immunomodulator; osteoporosis; cancer; cachexia; arthritis; cytostatic; osteopathic; therapy; human.
                                                            Human IL-6Ralpha-Fc
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                                                                                                                                                                                                                                                                                                                                                                                              VPPGEDSKDVAAPHROPLTSSERIDKQIRYILDGISALRKETCNKSNMCE--SSKEALAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention provides a novel fusion polypeptide capable of binding a cytokine to form a nonfunctional complex. The invention is useful for identifying agonists or antagonists of cytokine receptors for treating cytokine-related diseases or disorders e.g. cancer, cachexia, arthritis and osteoporosis. The present sequence is human I cachexia, arthritis and osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid molecules encoding fusion polypeptides capable of binding a cytokine to form a non-functional complex, useful for troptokine-related diseases or disorders, e.g. cancer, cachexia, art.
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22-MAR-2001;
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(YANC/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US2003143697-A1
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301
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                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                        VLRKPAAGSHPSRWAGMGRRLLLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPEEPQLS
                                                                                                                                                                                                                                                                                                                                   MLAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHW
                  PEGDSSFYIVSMCVASSVGSKFSKTQTFQGCGILQPDPPANITVTAVARNPRWLSVTWQD
                                                                                                                                                                                       CFRKSPLSNVVCEWGPRSTPSLTTKAVLLVRKFQNSPAEDFQEPCQYSQESQKFSCQLAV
                                                                                                                                                                                                                     CFRKSPLSNVVCEWGPRSTPSLTTKAVLLVRKFQNSPAEDFQEPCQYSQESQKFSCQLAV
                                                                                                                                                                                                                                                   ULRKPAAGSHPSRWAGMGRRLLLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPEEPQLS
                                                                                                                                                                                                                                                                                                                 MVAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHW
 GEWSEWSPEAMGTPWTESRSPPAENEVSTPMQALTTNKDDDNILFRDSANATSLPVQ---
                                                              PHSWNSSFYRLRFELRYRAERSKTFTTWMVKDLQHHCVIHDAWSGLRHVVQLRAQEEFGQ
                                                                                  PHSWNSSFYRLRFELRYRAERSKTFTTWMVKDLQHHCVIHDAWSGLRHVVQLRAQEEFGQ
                                                                                                                           PEGDSSFYIVSMCVASSVGSKFSKTQTFQGCGILQPDPPANITVTAVARNPRWLSVTWQD
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                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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2001US-00787835.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Inter-chain disulphide bridge"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Ala-Gly bridge"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 label Signal peptide
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                                                                                                                                                                                                                                                                                                                                                                            67.1%; Score 1921; DB 7; 77.1%; Pred. No. 4.2e-120; tive 22; Mismatches 44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Human mature IL-6Ralpha-Fc protein"
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useful for treating cachexia, arthritis,

and

Length 592; Indels 46;

Gaps

180

180

240

300 300 240 120

60

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RESULT 10
RAP90284
ID AAP90284
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                                                              Query Match
Best Local S
Matches 360
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04-AUG-1988;
14-JAN-1989;
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31-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAP90284 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAP90284;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Region
                                                                                                                                                                                                                                                                                                                                    Receptor protein for human B cell stimulating factor-2 - obtd. recombinant DNA techniques and used as diagnostic prophylactic therapeutic agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-JAN-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-JUL-1989
                                                                                                                                                                                        The cDNA in AAN90340 was derived from monocyte cell line U937. Isolated BSF2 receptor and DNA encoding it are claimed, as are (b) expression vectors; (c) host organisms; (d) antibodies; and (e) hybridomas. (Update on 25-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-JAN-1988;
                                                                                                                                                                                                                                                                                                  Claim 2;
                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kishimoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (KISH/) KISHIMOTO
                                                                                                                                                  Sequence
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                                                                  360;
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                                                                                                                                                                                                                                                                                                                                                                                                                               AAN90340.
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                                                                                      Similarity
                                                                                                                                                                                                                                                                                              Page 19-21; 63pp; English.
                                                                                                                                                      468
MLAVGCALLAALLAAPGAALAPRSCPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHW
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                                                                    Conservative
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88JP-00012599.
88JP-00194885.
89JP-00007461.
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/label= hy
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96.5%;
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                                                                       Score 1918; DB 1;
Pred. No. 5e-120;
1; Mismatches 4;
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                                                                                                              Length 468;
                                                                           Indels
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(Updated
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                                                                                                                                                                                                                                                                                                                                       Interleukin-6; IL-6; receptor; immunoglobulin-like; domain; truncat transmembrane; multiple myeloma; binding; ability; signal transfer; disease; intracellular.
                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR37215
                                                                                                                                                                                                                                                                                                                                                                                                                          AAR37215;
                                           This sequence represents an interleukin-6 (IL-6) receptor. Varien the receptor lacking either the immunoglobulin-like domain or the transmembrane and intracellular domain have IL-6 binding ability signal transfer ability. Either the full length or truncated IL-6 signal transfer ability. Bither the full length or truncated IL-6 receptors may be used for diseases caused by IL-6 such as multiply
                                                                                                                                                              WPI; 199
N-PSDB;
                                                                                                                                                                                                                                                                                                   JP05091892-A.
                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                  IL-6 receptor
                                                                                                                                                                                                                                                                                                                                                                                                      13-SEP-1993
                                                                                                                                                                                                                                                          02-OCT-1991;
                                                                                                                                                                                                                                                                              16-APR-1993.
                                                                                                                             New interleukin-6 receptor deriv. e.g. multiple myeloma.
                                                                                                                                                                                                                                     02-OCT-1991;
                                                                                                          Disclosure; Page 10-12;
                                                                                                                                                                                           (KISH/) KISHIMOTO C.
(CHUS ) CHUGAI PHARM
(TOYJ ) TOSOH CORP.
              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CFRKSPLSNVVCEWGPRSTPSLTTKAVLLVRKFQNSPAEDFQEPCQYSQESQKFSCQLAV 180
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Score
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1918;
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2
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Length 468;
                                                      as multiple
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Query Match

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RESULT 12
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The present invention describes a composition (I) comprising a recombinant DNAX cytokine receptor subunit-2 (DCRS2) polypeptide. The DCRS2 polypeptide is useful for binding ligands and for preparing antibodies. The DCRS2 polypeptide is also useful for modulating cell proliferation, for diagnostic and therapeutic applications, for detecting
                                                                                                                                                                                                       Novel composition comprising DNAX cytokine receptor subunit useful for regulating immune system function and for treatin immunological disorders.
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Best Local Simi
Matches 360;
                White J,
Barber R;
                                                                                                                                                                                                                                         Hypoxia-regulated condition; tumourigenesis; angiogenesis; retinopathy; inflammation; apoptosis; erythropoiesis; peripheral arterial disease; cancer; ischaemia; coronary arterial disease; inflammatory condition; rheumatoid arthritis; reperfusion injury; neonatal stress; infection; stroke; preeclampsia; atherosclerosis; cystic fibrosis; wound healing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  presence of their ligands and in drug screening assays. It is also useful for treating conditions such as immunological disorders. The present sequence represents a cytokine receptor subunit protein which is given in an alignment of various cytokine receptor subunits in the exemplification of the present invention
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                                                                                    22-FEB-2001; 2001GB-00004440.
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RESULT 14
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N-PSDB; AAD45938.
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                                                                                                                                       ABB78191 standard; protein;
 Human; interleukin-6; IL-6 receptor alpha; IL-^R alpha; IL-6; hepatocyte;
                                  Amino acid sequence of human interleukin-6 (IL-6) receptor alpha.
                                                                      05-NOV-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CFRKSPLSNVVCEWGPRSTPSLTTKAVLLVRKFQNSPAEDFQEPCQYSQESQKFSCQLAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          comprises administering to a human patient a soluble active agent which inhibits 0 interaction between human II-6 and hepatocytes, and so inhibits activation of glycoprotein 130 (gp130) and the internalisation of HBV into the hepatocytes. The soluble agent is selected from glycoprotein 80 (gp80), or its portion spanning amino acids 113-323 and having receptor sites that interact with II.6 and competitively inhibit interaction between II-6 and hepatocytes; glycoprotein 130 (gp130), or its portion spanning amino acids 1-94 and 141-230 and having receptor sites that interact with II-6 and competitively inhibit interaction between II-6 and competitively inhibit interaction between II-6 and competitively inhibit interaction between II-6 and hepatocytes; II-6 peptides IVS41-ALA56, GIY77-GIU95 or GIN153-HIS165; and/or a combined betal and beta2 II-6 mutant. The method is used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Inhibiting or treating infection of hepatocytes by hepatitis B virus using soluble agent which inhibits interaction between hIL-6 and hepatocytes, particularly hyper-IL-6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hepatitis B virus; HBV; glycoprotein 130; gp130; glycoprotein 80; gp80; hepatitis B infection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents a human interleukin-6 (IL-6) receptor alpha (IL-6R alpha). Fragments of IL-6 are used in the method of the invention. The specification describes a method for inhibiting or treating infection of hepatocytes by hepatitis B virus (HBV). The method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 9a-b; 38pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           prevent or treat hepatitis B infection
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                                                                                                                                                                       PEGDSSFYIVSMCVASSVGSKFSKTQTFQGCGILQPDPPANITVTAVARNPRWLSVTWQD
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                    GEWSEWSPEAMGTPWTESRSPPAENEVSTPMQALTTNKDDDNILFRDSANATSLPVEFMP
                                                                         PHSWNSSFYRLRFELRYRAERSKTFTTWMVKDLQHHCVIHDAWSGLRHVVQLRAQEEFGQ
                                                                                            PHSWNSSFYRLRFELRYRAERSKTFTTWMVKDLQHHCVIHDAWSGLRHVVQLRAQEEFGQ
                                                                                                                                               PEGDSSFYIVSMCVASSVGSKFSKTOTFQGCGILQPDPPANITVTAVARNPRWLSVTWQD
                                                                                                                                                                                                                    CFRKSPLSNVVCEWGPRSTPSLTTKAVLLVRKFQNSPAEDFQEPCQYSQESQKFSCQLAV
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                                                                                                                                                                                      GR molecule. Administration of the fusion protein results in the increased expression of one or more of MIP-lalpha, MIP-lbeta, RANTES or IP-10. Also claimed are a nucleic acid molecule encoding the fusion protein, an expression vector, a host cell, and a method of producing the fusion protein in the host cell. The fusion protein, nucleic acid or vector can be used in the manufacture of a medicament for the prophylaxis or treatment of an infectious disease (especially AIDS caused by a M-trophic strain of HIV, or bacterial peritonitis), an inflammatory disorder or an immunological disorder (especially rheumatoid arthritis), when it is desirable to increase or resolve an immune response (claimed)
                                                                                                                                                                                                                                                                                                                                                The present sequence is the protein sequence of the human interleukin-6 receptor (IL-6R). A soluble receptor is obtained either through proteolytic cleavage or differential mRNA splicing splicing of IL-6R (see ABP72698). The present invention relates to a fusion protein (see ABP72702) comprising a functional IL-6 molecule and a functional DS-sIL-ABP72702)
                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig
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antirheumatic; antiarthritic; antiinflammatory; immunosuppressive;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fusion protein having a functional IL-6 and DS-sIL-6R molecule, ful for the manufacture of a medicament for the prophylaxis or atment of an infectious disease, and an inflammatory or immunological
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Pred. No. 5e-120;
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                                                                                                                                                                                                                                                                               Composition potentially useful for treating immunological disorders, comprises a DNAX cytokine receptor subunit 2 (DCRS2) polypeptide, a natural DCRS2 polypeptide, or a fusion polypeptide comprising a DCRS2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNAX cytokine receptor subunit 2; DCRS2; cell physiology; cell development; cell culture; interferon detection; immune system disorder; interleukin 6; IL-6; receptor subunit alpha;
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31-MAY-2000; 2000US-00588113.
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BAZAN J F.
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The invention describes a composition of matter (I) comprising a substantially pure or recombinant DNAX cytokine receptor subunit 2 (DCRS2) polypeptide, a natural CRRS2 polypeptide, or a fusion protein comprising a DCRS2 sequence. A composition of matter comprises: a substantially pure or recombinant DCRS2 polypeptide comprising at least three distinct nonoverlapping segments of at least four amino acids

least

Disclosure;

SEQ

ID NO 12; 41pp; English.

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RESULT 17
AAY92195
ID AAY92195
AC AAY92
XX AAY92
XX II-AH
DT 01-AH
XX II-6R
KW II-6R
KW II-6R
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XX Synth
OS Synth
OS Homo
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 468
                                                                                                                                                                                                                                                                                                                                                                AAY92195 standard; protein; 690
                                   Protein
                                                                  Peptide
                                                                                                      Protein
                                                                                                                                                                        Synthetic
                                                                                                                                                                                                           IL-6R-alpha-C-gamma-1; cytokine; antagonist;
fusion protein; cytostatic; immunomodulator;
                                                                                                                                                                                                                                                           Human IL-6R-alpha-C-gamma-1 fusion protein.
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                                                                                                                                                                                                         cytostatic;
                                                  359. .360
/note= "Ala-Gly bridge"
                                                                         /label= IL-6R-alpha
                                                                                                                      Location/Qualifiers
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96.5%;
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Pred. No. 5e-120;
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                                                                                                                                                                                                           CNTF; receptor; osteopathic.
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The invention concerns production of antagonists to any cytokine that cutilizes an alpha specificity determining component, which when combined with the cytokine, binds to a first beta signal transducing component to form a non-functional intermediate which then binds to a second beta calphal transducing component causing beta-receptor dimerization, the cytokine alpha specificity determining component of the receptor (sr-calpha) and the extracellular domain of the first beta signal transducing component of the cytokine receptor (beta-1) are combined to form component of the cytokine by cytokine to form a non-functional complex. The receptor components are shared by cytokines such as the CNTF (ciliary neurotrophic development of II-6 antagonists, as they show that if, in the presence of cytokines, the invention provides the basis for the cytokine antagonists, as they show that if, in the presence of cytokine, it is alpha receptor and its beta-1 receptor component, can be cytokine it alpha receptor and its beta-1 receptor component, can be cytokine of the alpha specificity determining components of the extracellular domains of the ligand, it salpha specificity determining components of the cytokine conforms of the alpha specificity determining components of the cytokine conforms of the interacellular domains of specificity determining components of the cytokine conforms of the interacellular domains of specificity determining components of the cytokine conforms of their receptor. The nucleic acids and cytokine are useful for treating cytokine-related diseases or conservable myeloma or cachexia.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated nucleic acid molecule for treating cytokine-related diseases disorders encodes a fusion polypeptide capable of binding a cytokine t form a nonfunctional complex.
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19-MAY-1999;
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                                                                Sequence
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Score 1917; DB 3;
Pred. No. 9.4e-120;
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                 PHSWNGSFYRLRFELRYRAERSKTFTTWMVKDLQHHCVIHDAWSGLRHVVQLRAQEEFGQ 300
                                                                    PEGDSSFYIVSMCVASSVGSKFSKTQTFQGCGILQPDPPANITVTAVARNPRWLSVTWQD
                                                                                                           CFRKSPLSNVVCEWGPRSTPSLTTKAVLLVRKFQNSPAEDFQEPCQYSQESQKFSCQLAV
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PHSWNSSFYRLRFELRYRAERSKTFTTWMVKDLQHHCVIHDAWSGLRHVVQLRAQEEFGQ
                                                     PEGDSSFYIVSMCVASSVGSKFSKTQTFQGCGILQPDPPANITVTAVARNPRWLSVTWQD
                                                                                                                                                                                                                                                                               Conservative
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The invention concerns production of antagonists to any cytokine that utilizes an alpha specificity determining component, which when combined with the cytokine, binds to a first beta signal transducing component to form a non-functional intermediate which then binds to a second beta signal transducing component causing beta receptor dimerization, the soluble alpha specificity determining component of the receptor (sralpha) and the extracellular domain of the first beta signal transducing
                                                                                                                                                                                                                                                                             Isolated nucleic acid molecule for treating cytokine-related diseases disorders encodes a fusion polypeptide capable of binding a cytokine of
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19-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IL-6R-alpha-C-gamma-1; cytokine; antagonist;
fusion protein; cytostatic; immunomodulator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human IL-6R-alpha-kappa fusion protein
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                                                                                                                                                                                                                                                             nonfunctional complex.
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99US-00313942.
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rheumatoid arthritis; endotoxic

sapiens

Interleukin-6; IL; Interleukin-6 receptor.

L; receptor; antisense oligonucleotide; inhibition; kidney tumour; myeloma; Kaposi's sarcoma; psoriasi

psoriasis;

expression;

28-NOV-1996 AAR98364;

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AAR98364 standard;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CC component of the cytokine receptor (beta-1) are combined to form CC checked with the cytokine by combined to form the cytokine to form a non-functional complex. The receptor CC components are shared by cytokines such as the CNTF (ciliary neurotrophic CC factor) family of cytokines. The invention provides the basis for the CC development of IL-6 antagonists, as they show that if, in the presence of CC a ligand, a non-functional intermediate complex, consisting of the CC ligand, it will effectively block the action of the ligand. Effective antagonists of IL-6 or CNTF consist of heterodimers of the extracellular CC domains of the alpha specificity determining components of their cceptors and the extracellular domain of gpl30. The resultant CC receptors and the extracellular domain of gpl30. The resultant CC inaccessbile to form a signal transducing components of the native comborane-bound forms of their receptor. The nucleic acids and CC polypoptides are useful for treating cytokine-related diseases or CC disorders such as osteoporosis and primary and secondary effects of cancer including multiple myeloma or cachexia
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Best Local Simi
Matches 373;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          VLRKPAAGSHESRWAGMGRRLLLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPEEEPQLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MLAVGCALLAALLAAPGAALLAPRRCPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHW
 --YPREAKVOWKVDNALOSGNSOES 416
                                                                                                                                          GEWSEWSPEAMGTPWTESRSPPAENEVSTPMQALTTNKDDDNILFRDSANATSLPVQ---
                                                                                                                                                                 PEGDSSFYIVSMCVASSVGSKFSKTQTFQGCGILQPDPPANITVTAVARNPRWLSVTWQD
                                                                                                                                                                                                                                                                                                               PEGDSSFYIVSMCVASSVGSKFSKTQTFQGCGILQPDPPANITVTAVARNPRWLSVTWQD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MVAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHW
                                   LNLPKMA----EKDGCFQSGFNEET 441
                                                                                                       VPPGEDSKDVAAPHRQPLTSSERIDKQIRYILDGISALRKETCNKSNMCESSKEALAENN 420
                                                                                                                                                                                                                    PHSWNSSFYRLRFELRYRAERSKTFTTWMVKDLQHHCVIHDAWSGLRHVVQLRAQEEFGQ
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                                                                     ---DAGSGTVAAPSVFIFPPS---DEQLK---
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83.8%;
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Pred. No. 7.3e-1
1; Mismatches
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Matches 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antisense oligonucleotides may be used to inhibit the expression of the interleukin-6 receptor. Inhibition of expression of the II-6 receptor in useful in the treatment of kidney tumours, myeloma, Kaposi's Barcoma, rheumatoid arthritis, psoriasis and endotoxic shock. The antisense oligonucleotides are administered at a dosage of 0.1-100mg/kg, pref. O.
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18-AUG-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anti-sense oligo:nucleotide inhibitor against human IL-6R expression for treatment of e.g. tumours, cancers, rheumatoid arthritis, psorias endo:toxic shock, etc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 2; Page 17-21; 32pp; Japanese.
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                                                       ABP72699
            11-JUN-2003
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DB; AAT31441.
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                                                                                                                                                        GEWSEWSPEAMGTPWTESRSPPAENEVSTPMQALTTNKDDDNILFRDSANATSLPV----
                                                                                                                                                                      PHSWNSSFYRLRFELRYRAERSKTFTTWMVKDLQHHCVIHDAWSGLRHVVQLRAQEEFGQ
                                                                                                                                    VPPGEDSKDVAAP 373
                                                         standard;
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95JP-00210739.
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                                                        protein;
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Pred. No. 7.9e-120;
2; Mismatches 4;
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VLRKPAAGSHPSRWAGMGRRLLLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPEBPQLS

180

120

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CFRKSPLSNVVCEWGPRSTPSLTTKAVLLVRKFQNSPAEDFQEPCQYSQESQKFSCQLAV | CFRKSPLSNVVCEWGPRSTPSLTTKAVLLVRKFONSPAEDFQEPCQYSQESQKFSCQLAV

181

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GEWSEWSPEAMGTPWTESRSDPAENEVSTPMQALTTNKDDDNILFRDSANATSLPVE 357

GEWSEWSPEAMGTPWTESRSPPAENEVSTPMQALTTNKDDDNILFRDSANATSLPVQ

PHSWNSSFYRLRFELRYRAERSKTFTTWMVKDLQHHCVIHDAWSGLRHVVQLRAQEEFGQ PEGDSSFYIVSMCVASSVGSKFSKTQTFQGCGILQPDPPANITVTAVARNPRWLSVTWQD PEGDSSFYIVSMCVASSVGSKFSKTQTFQGCGILQPDPPANITVTAVARNPRWLSVTWQD

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PHSWNSSFYRLRFELRYRAERSKTFTTWMVKDLQHHCVIHDAWSGLRHVVQLRAQEEFGQ

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                                                                                                     Matches
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Best Local 9
                                                                                                                                                                                     The present sequence is the protein sequence of a soluble form of the human interleukin-6 receptor (IL-6R), denoted PC-SIL-6R, produced by proteolytic cleavage. A fusion protein of human IL-6 and PC-SIL-6R increases expression of MCP-1, but unlike a novel fusion protein of the invention (see Ampr2702) comprising IL-6 and DS-SIL-6R, does not increase expression of MIP-1alpha, MIP-1beta, RANTES or IP-10. The invention relates to this novel fusion protein and its use in the prophylaxis or relates to this novel fusion protein and its use in the prophylaxis or treatment of an infectious disease (especially AIDS caused by a M-trophic strain of HIV, or bacterial peritonitis), an inflammatory disorder or an immunological disorder (especially rheumatoid arthritis), when it is desirable to increase or resolve an immune response
                                                                                                                                                                                                                                                                                                                                                                                                        New fusion protein having a functional IL-6 and DS-sIL-6R molecule, useful for the manufacture of a medicament for the prophylaxis or treatment of an infectious disease, and an inflammatory or immunolo disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; interleukin-6; receptor; PC-sIL-6R; antibacterial; virucide;
anti-HIV; antirheumatic; antiarthritic; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Soluble interleukin-6 receptor isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-AUG-2001; 2001GB-00019015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-AUG-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-FEB-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO2003014359-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UYCA-) UNIV COLLEGE CARDIFF: (UYWA-) UNIV WALES COLLEGE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immunosuppressive;
                                                                                                                                                             Sequence 357 AA;
                                                                                                                                                                                                                                                                                                                                                                            Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2003-256588/25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SA,
                                                                                                   356;
            61
                                                             1 MLAVGCALLAALLAADGAALAPRRCPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHW
                                         ш
                                                                                                                     Similarity
VLRKPAAGSHPSRWAGWGRRLLLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPEEPQLS
                                           MLAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Topley N;
                                                                                                                                                                                                                                                                                                                                                                           Fig
                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2002WO-GB003581
                                                                                                                                                                                                                                                                                                                                                                              2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene
                                                                                                                                                                                                                                                                                                                                                                              46pp;
                                                                                                                     66.9%;
99.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   therapy.
                                                                                                                                                                                                                                                                                                                                                                                English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ç
                                                                                                     ۲,
                                                                                                      Score 1913; DB 6;
Pred, No. 7.7e-120;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDICINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PC-sIL-6R
                                                                                                           0,
                                                                                                                                       Length
                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              or immunological
                                                                                                                                          357;
                                                                                                           0,
                                                                                                             Gaps
                    120
                                                   60
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11

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RESULT 21
AAY92197
ID AAY922
XX AAY92
XX AAY92
XX O1-AU
XX IL-6R
KW Fusio
OS Synth
OS Homo
OPN W0200
XX Fusion
PF 22-SE
XX APP
PF 22-SE
XX APP
PF 22-SE
XX APP
PF 22-SE
XX APP
PF 19-M
XX IL-6R
PF 19-M
XX IL-6R
RW Fusion
PF 22-SE
XX ISOLUTION
PF 19-M
XX ISOLUTION
PF 19-M
XX ISOLUTION
PF 1801
XX ISOLUTION
   밁
                                                     S
                                                                                                                                                                                                                                                                                                        CC component of the cytokine receptor (beta-1) are combined to form
CC heterodimers (8R-alpha:beta-1) that act as antagonist to the cytokine by
CC binding the cytokien to form a non-functional complex. The receptor
CC components are shared by cytokines such as the CNTF (ciliary neurotrophic
CC factor) family of cytokines. The invention provides the basis for the
CC development of II-6 antagonists, as they show that if, in the presence of
CC aligand, a non-functional intermediate complex, consisting of the
CC ligand, it will effectively block the action of the ligand. Effective
CC formed, it will effectively block the action of the ligand. Effective
CC antagonists of II-6 or CNTF consist of heterodimers of the extracellular
CC domains of the alpha specificity determining components of their
CC receptors and the extracellular domain of gpl30. The resultant
CC inaccessbile to form a signal transducing complex with the native
CC membrane-bound forms of their receptor. The nucleic acids and
CC polypeptides are useful for treating cytokine-related diseases or
CC cancer including multiple myeloma or cachexia
                                                                                                                              Query Match
Best Local S
Matches 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention concerns production of antagonists to any cytokine that utilizes an alpha specificity determining component, which when combined with the cytokine, binds to a first beta signal transducing component to form a non-functional intermediate which then binds to a second beta signal transducing component causing beta-receptor dimerization, the soluble alpha specificity determining component of the receptor (sralpha) and the extracellular domain of the first beta signal transducing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated nucleic acid molecule for treating cytokine-related diseases or disorders encodes a fusion polypeptide capable of binding a cytokine to form a nonfunctional complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 4; Page; 152pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-293165/25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stahl N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200018932-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human IL-6R-alpha-j-kappa fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY92197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY92197 standard; protein;
                                                                                                                                                                                                                                                      Sequence 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-SEP-1998;
19-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IL-6R-alpha-j-kappa; cytokine; antagonist; CNTF; receptor; fusion protein; cytostatic; immunomodulator; osteopathic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (REGE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sapiens
                                                                                                                              al Similarity
375; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGENERON PHARM INC
Yancopoulos GD;
                                                                                                                                                                                                                                                         AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-0101858P.
99US-00313942.
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                                                                                                                                                         66.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      477
                                                                                                                           Score 1912; DB 3;
Pred. No. 1.3e-119;
3; Mismatches 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Š
                                                                                                                                                                                       Length 477;
                                                                                                                              40;
                                                                                                                              Gaps
      60
                                                               60
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RESULT 22
AAW70804
ID AAW70
XX AAW70
XX AAW70
XX AAW70
XX AM1no
XX GP130
KW GP130
KW GP130
XX GP140
XX GP140
XX GP140
XX GP140
XX GP140
XX GP150
XX GP160
XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ś
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              닭
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S
                   The present sequence represents the amino acid sequence of interleukin (IL)-6R-alpha domain. The protein is used in the course of the inventic The specification describes cytokine antagonists comprising only the extracellular domain of the specificity-determining component of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW70804 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     granulocyte macrophage colony-stimulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW70804;
                                                                                                                                                                                                                  Cytokine antagonists - comprising edetermining and signal-transducing
                                                                                                                                                                                                                                                                                                 WPI; 1999-044669/04.
                                                                                                                                                                                                                                                                                                                                                    Yancopoulos
                                                                                                                                                                                                                                                                                                                                                                                                         (REGE-) REGENERON PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-OCT-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US5844099-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transforming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gp130; cytokine antagonist; interleukin; gamma-interferon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Amino acid sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121
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                                                                                                                                                             4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GEWSEWSPEAMGTPWTESRSPPAENEVSTPMQALTTNKDDDNILFRDSANATSLPVE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CFRKSPLSNVVCEWGPRSTPSLTTKAVLLVRKFQNSPAEDFQEPCQYSQESQKFSCQLAV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VLRKPAAGSHPSRWAGMGRRLLLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPEEPQLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PHSWNSSFYRLRFELRYRAERSKTFTTWMVKDLQHHCVIHDAWSGLRHVVQLRAQEEFGQ 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CFRKSPLSNVVCEWGPRSTPSLTTKAVLLVRKFQNSPAEDFQEPCQYSQESQKFSCQLAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KEALAENNLNLPKWA----EKDGCFQSGFNEET 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TF-----GQGTKVEIKTVAAPSVFIFPPS---DEQLK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GEWSEWSPEAMGTPWTESRSPPAENEVSTPMQALTTNKDDDNILFRDSANATSLPVQDAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PHSWNSSFYRLRFELRYRAERSKTFTTWMVKDLQHHCVIHDAWSGLRHVVQLRAQEEFGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PEGDSSFYIVSMCVASSVGSKFSKTQTFQGCGILQPDPPANITVTAVARNPRWLSVTWQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PEGDSSFYIVSMCVASSVGSKFSKTQTFQGCGILQPDPPANITVTAVARNPRWLSVTWQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VLRKPAAGSHPSRWAGMGRRULLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPEEPQLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -FMPVPPGE----DSKDVAAPHRQPLTSSERIDKQIRYILDGISALRKETCNKSNMCESS
                                                                                                                                                          Fig
                                                                                                                                                                                                                                                                                                                                                    GD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first
                                                                                                                                                             15; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93US-00140222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95US-00563105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---YPREAKVQWKVDNALQSGNSQES 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                    Stahl N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               factor-beta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "soluble interleukin (IL)-6R-alpha domain"
                                                                                                                                                                                                                  comprising extracellular domains of specificity-transducing components of cytokine receptor.
                                                                                                                                                                                                                                                                                                                                                       Economides A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       interleukin (IL)-6R-alpha domain.
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The specification describes cytokine antagonists comprising only the extracellular domain of the specificity-determining component of the cytokine receptor and the extracellular domain of a signal-transducing

the invention.

Example 4; Fig 15; 152pp; English

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RESULT 23
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                         Isolated nucleic acid molecule for treating cytokine-related diseases disorders encodes a fusion polypeptide capable of binding a cytokine t form a nonfunctional complex.
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                                                                                                                                                                                                                                                                                                     25-SEP-1998;
19-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Soluble II-6-R-alpha; cytokine; antagonist; CNTF; receptor; fusion protein; cytostatic; immunomodulator; osteopathic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Soluble human IL-6-R-alpha
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99US-00313942.
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Pred. No. 1.2e-119;
2; Mismatches 0;
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Sequence 360 AA;

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                                     The invention concerns production of antagonists to any cytokine that cutilizes an alpha specificity determining component, which when combined component of the cytokine, binds to a first beta signal transducing component to component a non-functional intermediate which then binds to a second beta component to the cytokine receptor dimerization, the component of the extracellular domain of the first beta signal transducing component of the cytokine receptor (beta-1) are combined to form component of the cytokine receptor (beta-1) are combined to form component of the cytokine receptor (beta-1) are combined to form components are shared by cytokines such as antagonist to the cytokine by cytokines such as the CNTF (ciliary neurotrophic factor) family of cytokines. The inventional complex. The receptor component of II-6 antagonists, as they show that if, in the presence of cytokines, the invention provides the basis for the cytokine, it salpha receptor and its beta-1 receptor component, can be cytokines of the alpha specificity determining components of the extracellular domain of gpl30. The resultant cytokines for the antagonists of the alpha specificity determining components of the extracellular domain of gpl30. The resultant cytokine are useful for treating cytokine realeting the cytokine components such as signal transducing complex with the native components such as osteoporosis and primary and secondary effects of cancer including multiple myeloma or cachexia
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GEWSEWSPEAMGTPWTESRSPPAENEVSTPMQALTTNKDDDNILFRDSANATSLPVQ
                     GEWSEWSPEAMGTPWTESRSPPAENEVSTPMQALTTNKDDDNILFRDSANATSLPVE 357
                                                                                              PHSWNSSFYRLRFELRYRAERSKTFTTWMVKDLQHHCVIHDAWSGLRHVVQLRAQEEFGQ 300
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99.4%;
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RESULT 24
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                             Cytokine; cytokine-related disease; immunomodulator; osteoporosis; cancer; cachexia; arthritis; cytostatic; osteopathic; therapy; hum
  Homo sapiens
                                                                       Human IL-6Ralpha-domain protein.
                                                                                                   12-FEB-2004
                                                                                                                               ABW02172
                                                                                                                                                       ABW02172 standard; protein; 360
                                                                                                 (first
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RESULT 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention provides a novel fusion polypeptide capable of binding a cytokine to form a nonfunctional complex. The invention is useful for identifying agonists or antagonists of cytokine receptors an for treating cytokine-related diseases or disorders e.g. cancer, cachesia, arthritis and osteoporosis. The present sequence is human IL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid molecules encoding fusion polypeptides capable of binding a cytokine to form a non-functional complex, useful for treating cytokine-related diseases or disorders, e.g. cancer, cachexia, arthritis,
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 360 AA;
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22-MAR-2001; 2001US-00787835.
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                        AAP90525 standard;
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                                                                                                                                                                                                                                               CFRKSPLSNVVCEWGPRSTPSLTTKAVLLVRKFQNSPAEDFQEPCQYSQESQKFSCQLAV
                                                                                                                                                                                                                                                                                                                               VLRKPAAGSHPSRWAGMGRRLLLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPEEPQLS
                                                                                                                                                                                                                                                                                               VLRKPAAGSHPSRWAGMGRRLLLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPEEPQLS
                                                                                                    GEWSEWSPEAMGTPWTESRSPPAENEVSTPMQALTTNKDDDNILFRDSANATSLPVE 357
                                                                                                                                                  PHSWNSSFYRLRFELRYRAERSKTFTTWMVKDLQHHCVIHDAWSGLRHVVQLRAQEEFGQ
                                                                                                                                                                                  PEGDSSFYIVSMCVASSVGSKFSKTQTFQGCGILQPDPPANITVTAVARNPRWLSVTWQD
                                                                                                                                                                                             PEGDSSFYIVSMCVASSVGSKFSKTQTFQGCGILQPDPPANITVTAVARNPRWLSVTWQD
                                                                                                                                                                                                                                  CFRKSPLSNVVCEWGPRSTPSLTTKAVLLVRKFQNSPAEDFQEPCQYSQESQKFSCQLAV
                                                                                                                                                                                                                                                                                                                                                                                Conservative
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99. .100
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                        protein; 468 AA
                                                                                                                                                                                                                                                                                                                                                                                           66.8%;
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                                                                                                                                                                                                                                                                                                                                                                                           Score 1910; DB 7;
Pred. No. 1.2e-119;
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RESULT 26 ABP72698 ID ABP7

ABP72698 standard; protein; 364

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Matches 359
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                                                                                                                                                                                                                                                                                                                                                                            The BSF2 receptor is derived from a monocyte U937 cell line. It can used to develop prophylactic and therapeutic pharmaceuticals, as age relate diseases and disorders to abnormal BSF-2 prodn. It can also used to study an immune mechanism with which BSF-2 or the receptor concerned. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Receptor protein for human B cell stimulatory factor-2 - used developing prophylactic, therapeutic and diagnostic agents for disorders.
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23-JAN-1990
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                                                                                                                                                                                                                                                                                                                                                         Sequence 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 2; Page 36; 76pp; English.
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N-PSDB; AAP90525.
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                                                                                                                                                                                                                                                                           1 MLAVGCALLAALLAADARGAALAPRRCPAQEVARGVLTSLPGDSVTLLTCPGVEPEDNATVHW
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                                                                                                                                                                                                                URKPAAGSHPSRWAGMGRRLLLRSVQLHDSGNYSCYRAERPAGTVHLLVDVPPEEPQLS
                                                                                                                                                                                                                              VLRKPAAGSHPSRWAGMGRRLLLLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPEEPQLS
                                                                                                                                                                                   CFRKSPLSNVVCEWGPRSTPSLTTKAVLLVRKFQNSPAEDFQEPCQYSQESQKFSCQLAV
                                             GEWSEWSPEAMGTPWTESRSPPAENEVSTPMQALTTNKDDDNILFRDSANATSLPVEFMP
                                                                                      PHSWNSSFYRLRFELRYRAERSKTFTTWMVKDLQHHCVIHDAWSGLRHVVQLRAQEEFGQ
                                                                                                                                    PEGDSSFYIVSMCVASSVGSKFSKTQTFQGCGILQPDPPANITVTAVARNPRWLSVTWQD
                                                                                                                                                                    CFRKSPLSNVVCEWGPRSTPSLTTKAVLLVRKFQNSPAEDFQEPCQYSQESQKFSCQLAV
                                                                                                                                                                                                                                                               VPPGEDSKDVAAP 373
                                                                          PHSWNSSFYRLRFELRYRAERSKTFTTWMVKDLQHHCVIHDAWSGLRHVVQLRAQEEFGQ
                                                                                                                       PEGDSSFYIVSMCVASSVGSKFSKTQTFQGCGILQPDPPANITVTAVARNPRWLSVTWQD
                               GEWSEWSPEAMGTPWTESRSPPAENEVSTPMQALTTNKDDDNILFRDSANATSLPV----
                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               factor-2 receptor; monocyte U937
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                                                                                                                                                                                                                                                                                                           Score 1910; DB 1;
Pred. No. 1.7e-119;
1; Mismatches 5;
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differential mRNA splicing. The invention relates to a fusion protein (see ABP72702) comprising a functional II-6 molecule and a functional DS-SIL-6R molecule. Administration the fusion protein results in the increased expression of one or more of MIP-labba, MIP-lbeta, RANTES or IP-10. High levels of MIP-labba, MIP-lbeta and RANTES complete with HIV for binding to CCR5 and effectively suppress HIV entry. The fusion protein can be used in the treatment of any disease in which the invention also provides a nucleic acid molecule encoding the fusion protein, an expression vector, a host cell, and a method of producing the fusion protein, an expression vector, a host cell, and a method of producing the fusion protein, an expression vector, a host cell, and a method of producing the fusion protein in the host cell. The fusion protein, nucleic acid or vector can be used in the manufacture of a medicament for the prophylaxis or treatment of an infectious disease (especially AIDS caused by a M-trophic strain of HIV, or bacterial peritonitis), an inflammatory disease or resolve an immune response (claimed) when it is desirable to increase or resolve an immune response (claimed)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 355;
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New fusion protein having a functional IL-6 and DS-sIL-6R molecule, useful for the manufacture of a medicament for the prophylaxis or treatment of an infectious disease, and an inflammatory or immunological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; interleukin-6; receptor; DS-sIL-6R; antibacterial; virucide; anti-HIV; antirheumatic; antiarthritic; antiinflammatory; immunosuppressive; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-AUG-2002; 2002WO-GB003581
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-JUN-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is the protein sequence of a soluble form of the human interleukin-6 receptor (IL-6R), denoted DS-sIL-6R, produced by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 4; 46pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                  1 MLAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHW
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                                                                                                                 CFRKSPLSNVVCEWGPRSTPSLTTKAVLLVRKFQNSPAEDFQEPCQYSQESQKFSCQLAV 180
                                                                                                                                                                                                       VLRKPAAGSHPSRWAGMGRRLLLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPEEPQLS
                                                                                                                                                                                                                                                                          VLRKPAAGSHPSRWAGMGRRLLLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPEEPQLS
                                                                                                                                                                                                                                                                                                                                           PEGDSSFYIVSMCVASSVGSKFSKTQTFQGCGILQPDPPANITVTAVARNPRWLSVTWQD 240
                                                                CFRKSPLSNVVCEWGPRSTPSLTTKAVLLVRKFQNSPAEDFQEPCQYSQESQKFSCQLAV
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                                                                                                                                                                                                                                                                                                                             This is a previously reported amino acid sequence for human interleukin-6 (C) (hIL-6) receptor alpha. The invention relates to the finding that hIL-6 (C) is essential for hepatitis B virus (HBV) infection. The invention (C) provides a pharmaceutical composition for the treatment of HBV infection, comprising a soluble active agent that interacts with at least one of the binding sites between hIL-6 and the pS1 region of HBV and between hIL-6 and hepatocytes and other HBV-permissive cells. The active agent competitively binds to at least one of these sites and thereby prevents thIL-6-mediated HBV infection of hepatocytes and other HBV-permissive cells. The soluble active agent is selected from glycoprotein 80 (gy80) having receptor sites which interact with hIL-6, bill-6 derived peptide Gln53-His165, a combined 1 and 2 hIL-6 mutant (mhIL-6 1+2), and mill-6 tysubstituted with Phel71 to Leu and Ser177 to Arg, and mixtures
                                                                                                                                                Query Match
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                                                                                                                      Matches
                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                          of any of these
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Treatment of hepatitis B virus infection - using a soluble active agent which prevents interaction of HBV with hepatocytes mediated by human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human interleukin-6 receptor alpha polypeptide
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                            1 MLAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHW
                                                                                                                                                   Similarity
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                                                                                                                                                66.4%;
                                                                                                                                             Score 1900; DB 2
Pred. No. 8e-119;
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This sequence represents the SR345 protein. The invention relates to a method for isolating a gene encoding a membrane-bound protein, comprising introducing a vector into a cell, contacting an antigen with the cell expressing the fused protein encoded by the vector on its surface to select an antigen-binding cell, and isolating the cDNA. The vector contains DNA encoding a secretable functional protein with antigenicity and binding affinity, and a cDNA ligated to DNA downstream of the 3' end of the coding sequence. The method can be used to isolate a membrane-bound protein for diagnosis and study. It can also be used for producing drugs treating abnormal functions of the protein. Such a technique is
                                                                                                                                                                                                                                                                                                                                                                                               Efficient and selective isolation of a gene encoding membrane puwith low or no antigenic binding activity, for diagnosis, study production of drugs treating abnormal functions of the protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gene isolation; membrane-bound protein; fusion protein; drug production; antigen-binding cell; secretable functional protein; antigenic protein; protein isolation; diagnosis; SR345 protein.
                                                                                                                                                                                                                                                                                                                                            Example 1; Page 49-52;
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01-OCT-1998;
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DB; AAZ40288.
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98JP-00279876.
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Matches 345
                                                                                          Receptor protein for human B cell stimulatory factor-2 - used developing prophylactic, therapeutic and diagnostic agents for disorders.
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Pred. No. 3.6e-116;
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The BSF2 receptor has amino acids at the C-terminal deleted. The receptor is derived from a monocyte U937 cell line. It can be used to develop prophylactic and therapeutic pharmaceuticals, as agents to relate diseases and disorders to abnormal BSF-2 prodn. It can also be used to

Claim 7;

Page

40;

English

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ARESULT 30
AAY92205
ID AAY92
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(Updated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IL-6 trap; cytokine; antagonist; CNTF; receptor; fusion protein; cytostatic; immunomodulator; osteonathic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fusion polypeptide 616, IL-6 trap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY92205 standard; protein;
                                                                                                                    Isolated nucleic acid molecule for treating cytokine-related diseases or disorders encodes a fusion polypeptide capable of binding a cytokine to
                                                                                                                                                                                                                                                               Stahl N,
                                                                                                                                                                                                                                                                                                                                                          25-SEP-1998;
19-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GEWSEWSPEAMGTPWTESRSPPAENEVSTPMQALTTNKDDDNIL 344
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Pred. No. 9e-116;
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cytokine II-6 to form a non-functional complex. The invention concerns component of antagonists to any cytokine that utilizes an alpha compectation of antagonists to any cytokine when combined with the cytokine, chinds to a first beta signal transducing component to form a non-combined with the cytokine, component components and components are cytokine to form a non-functional complex. The receptor components are cytokine to form a non-functional complex. The receptor components are cytokine to form a non-functional complex. The receptor components are cytokines. The invention provides the basis for the development of II-components, as they show that if, in the presence of a ligand, a non-functional intermediate complex, consisting of the ligand, its alpha components and its beta-1 receptor component, can be formed, it will component component components and the sectively block the action of the ligand. Effective antagonists of the alpha components of their receptors and the extracellular domains of the alpha components of their receptors and the components of the cytokine components of their receptors and the components of their receptors and the cytokine-related diseases or disorders such as osteoporosis and primary components of components of their receptors and the cytokine are useful for treating components of components of their receptors and primary components of components of components of their receptors and primary components of components of their receptors and the cytokine components of their receptors and 
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Matches 331;
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                                                                                                                                                                                                                                                                                                                                                                  standard;
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                                                                                                         GEWSEWSPEAMGTPWTESRSPPAENEVSTPMELL 334
                                                                                                                                     GEWSEWSPEAMGTPWTESRSPPAENEVSTPMQAL 334
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protein; 1158
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pred. No. 7.8e-111;
2; Mismatches 1;
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Homo sapiens
                                         Cytokine; cytokine-related disease;
                                                          Human cytokine trap-616 protein.
                                                                           12-FEB-2004
                                  cachexia;
                                                                            (first entry)
                                   arthritis;
                                  isease; immunomodulator; osteoporosis;
cytostatic; osteopathic; therapy; hum
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This sequence shows fusion polypeptide Example 6; Fig 25A-F; 152pp; English.

616, which

B.

capable of binding

US2003143697-A1

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RESULT 32
AAY92204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention provides a novel fusion polypeptide capable of binding a cytokine to form a nonfunctional complex. The invention is useful for identifying agonists or antagonists of cytokine receptors for treating cytokine-related diseases or disorders e.g. cancer, cachexia, arthritis and osteoporosis. The present sequence is human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid molecules encoding fusion polypeptides capable of binding a cytokine to form a non-functional complex, useful for treating cytokine-related diseases or disorders, e.g. cancer, cachexia, arthritis.
IL-6 trap; cytokine; antagonist; CNTF; re
cytostatic; immunomodulator; osteopathic.
                                                                                                                                  AAY92204 standard; protein; 1168 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cytokine trap protein
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22-MAR-2001; 2001US-00787835.
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                                          Fusion polypeptide 412, IL-6 trap
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YANCOPOULOS G
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This sequence shows fusion polypeptide 412, which is capable of binding cytokine II-6 to form a non-functional complex. The invention concerns cytokine II-6 to form a non-functional complex. The invention concerns cytokine in the cytokine, and the cytokine, and the cytokine of antagonists to any cytokine that utilizes an alpha cytokine intermediate which then binds to a second beta signal transducing component to form a non-cytokine intermediate which then binds to a second beta signal cytokine intermediate which then binds to a second beta signal cytokine specificity determining component of the receptor (sR-alpha) and cytokine specificity determining component of the receptor (sR-alpha) and cytokine specificity determining component of the receptor cytokine intermediate cytokine as the cytokine are combined to form heteroidments are cytokine to form a non-functional complex. The receptor components are cytokine by cytokines such as the CNTF (ciliary neurotrophic factor) family of cytokines. The invention provides the basis for the development of II-cytokines. The invention provides the basis for the development of II-cytokines are they show that if, in the presence of a ligand, a non-functional intermediate complex, consisting of the ligand, its alpha cytokine intermediate complex, consisting of the ligand, its alpha cytokine intermediate of the intermediate complex with the nation of their receptors and the extracellular domains of the alpha cytokine cytokine cytokine with the native membrane-bound forms of their components of their comp
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19-MAY-1999;
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Query Match Best Local S Matches 330 Similarity Conservative 62.3%; Score 1783; DB 3; Pred. No. 1.7e-110; 1; Mismatches 0; Length 1168; Indels

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Sequence

밁 ঠ 밁 Ś 밁 Ś 181 121 121 61 13 VLRKPAAGSHPSRWAGMGRRLLLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPEEPQLS WAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHW MLAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHW CFRKSPLSNVVCEWGPRSTPSLTTKAVLLVRKFQNSPAEDFQEFCQYSQESQKFSCQLAV VLRKPAAGSHPSRWAGMGRRLLLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPEEPQLS PEGDSSFYIVSMCVASSVGSKFSKTQTFQGCGILQPDPPANITVTAVARNPRWLSVTWQD CFRKSPLSNVVCEWGPRSTPSLTTKAVLLVRKFQNSPAEDFQEPCQYSQESQKFSCQLAV 180 120 120 60 240 180

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid molecules encoding fusion polypeptides capable of binding a cytokine to form a non-functional complex, useful for treating cytokine-related diseases or disorders, e.g. cancer, cachexia, arthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB;
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22-MAR-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                      The present invention provides a novel fusion polypeptide capable of binding a cytokine to form a nonfunctional complex. The invention is useful for identifying agonists or antagonists of cytokine receptors for treating cytokine-related diseases or disorders e.g. cancer, cachesia, arthritis and osteoporosis. The present sequence is human cytokine trap protein
                                                                                                                                                                                                                                                                                                                                                              Sequence
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achexia; arthritis; cytostatic; osteopathic; therapy; human.
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CFRKSPLSNVVCEWGPRSTPSLTTKAVLLVRKFQNSPAEDFQEPCQYSQESQKFSCQLAV
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179.
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Cytostatic; antiinflammatory; antirheumatic; antiarthritic; anti-HIV; nephrotropic; osteopathic; antipsoriatic; interleukin-6 receptor; IL-6R; alpha chain; cytokine; multiple myeloma; lymphoma; inflammation; sepsis; rheumatoid arthritis; prostate cancer; Castleman's disease; ALDS; human; mesangial proliferative glomerulonephritis; Kaposi's sarcoma; psoriasis; osteoporosis; protein co-ordinate data; wild-type.
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to form a homodimer"
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Domain
The invention relates to selecting or designing a compound that interacts with the interleukin-6 receptor (IL-6R) via assessing and obtaining the stereochemical complementarity between compound and a topographic region of the receptor and testing the compound for its ability to modulate an activity associated with the receptor. Also disclosed is the crystal structure of the IL-6R alpha chain. The compounds of the
                                                                                                                                                 Varghese JN,
Smith BJ;
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                                                                  Disclosure; Page 356-357; 361pp; English
                                                                                                                             WPI; 2003-558820/52.
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                                                                                                                                                                                                                    14-SEP-2001; 2001AU-00007695
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LUDWIG INST CANCER RES.
HALL INST MEDICAL RES WALTER &
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                                                                                                or designing compound interacting r treatment of e.g. AIDS, involves
                                                                                      modulate activity of
                                                                                                                                                          Simpson RJ,
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to form a homodimer"
284. .287
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/note=_"Forms a left-handed 310 helix structure"
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/note= "Forms a left-handed_310 helix structure"
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                                                                                               with interleukin receptor, assessing and testing
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Best Local Similarity
Matches 325; Conserv
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                                                                                                                                                                                                                                                                                                                                   16-OCT-2003
25-MAR-2003
                                                                                                                                                                                                                       Hybrid peptide; malaria parasite; Plasmodium falciparum; red blood cell; cytokine receptor; glycophorin binding pe GBP 130; GBPH; glycophorin binding peptide homologue; gly
                                                                                                                                                                                                                                                                                                                                                                                                                   AAR70122 standard;
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                                                WO9506737-A1
                                                                                                               Misc-difference
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Plasmodium f
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ng peptide 130
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09-MAR-1995

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An Hybrid peptides for binding cytokines, comprising a malaria parasite CC (Plasmodium falciparum) peptide (capable of binding to a red blood cell (RBC)) and a receptor peptide are claimed. R70103-25 are examples of CC (these hybrid peptides. R70122 is a fusion of interleukin 6 receptor (as CC confirmed with reference to SWISSPROT, as it is unclear in the CC specification whether this sequence is In6-R or In8-R typel) and CC glycophorin binding protein (GBP) 130. The use of cytokine receptors not CC RBC without deleterious effect. The RBC protects the hybrid peptides from RBC without deleterious effect. The RBC protects the hybrid peptides from CC excretion from the kidney, and due to steric hindrance prevents the excretion from the prefd. malaria parasite peptides used, others include homologue) are the prefd. malaria parasite peptides used, others include CC (SBA 175 (175 kDa erythrocyte binding antigen), PMWSA (pre major merozoite surface antigen) and the Duffy binding receptor molecule (eg. exhibited by Plasmodium vivax). These peptides hind to pref. glycophorin A, B and CC (Sialo glycoproteins, found on the surface of RBCs. The hybrid peptides CC are thus used to lower the levels of free cytokines in the circulation to CC (Updated on 16-OCT-2003 to standardise OS field)
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23-AUG-1994;
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parasite peptide capable of binding a red blood
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Pred. No. 6e-109;
5; Mismatches 73;
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The invention relates to selecting or designing a compound that interacts with the interleukin-6 receptor (II-6R) via assessing and obtaining the stereochemical complementarity between the compound and a topographic region of the receptor and testing the compound for its ability to modulate an activity associated with the receptor. Also disclosed is the crystal structure of the II-6R alpha chain. The compounds of the invention act as cytokine receptor modulators and may be useful in the prevention and treatment of diseases associated with signalling by II-6R such as multiple myeloma, inflammation, rheumatoid arthritis, prostate cancer, Castleman's disease, AIDS, mesangial proliferative glomerulonephritis, Kaposi's sarcoma, sepsis, osteoporosis and psoriasis.
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                                                                                                                                             Example 1;
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Smith BJ;
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(LUDW-)
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LUDWIG INST CANCER RES.
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                                                                                                                                                                 or designing compound interacting with interleukin receptor, r treatment of e.g. AIDS, involves assessing and testing to modulate activity of receptor.
                                                                                                                                            Page; 361pp;
                                                                                                                                                                                                                                                                            INST MEDICAL
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Matches 324; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The method provides enhanced stereochemical complementarity relative to the naturally occurring IL-6 receptor ligand as well as a rational basis for the development of ligands for specific therapeutic applications. The information provided by the IL-6R crystal structure will facilitate a more accurate understanding of how the binding of a ligand leads to signal transduction. The current sequence is that of the human IL-6R alpha chain mutant protein of the invention which contains a V259Q substitution. Note: The present sequence is not shown within the specification but was created by the indexer using the human IL-6R alpha chain will-tree created.
                                                                                                                                                                                                                                                 nephrotropic; osteopathic; antipsoriatic; interleukin-6 receptor; II-6R; alpha chain; cytokine; multiple myeloma; lymphoma; inflammation; sepais; rheumatoid arthritis; prostate cancer; Castleman's disease; AIDS; human; mesangial proliferative glomerulonephritis; Kaposi's sarcoma; psoriasis;
                                                                                                                                                                                                                                                                                                                                             Human interleukin 6 receptor alpha chain mutant peptide -
                                Domain
                                                            Disulfide-bond
                                                                                                          Domain
                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                  osteoporosis;
                                                                                                                                                                                                                                                                                                               Cytostatic; antiinflammatory; antirheumatic; antiarthritic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             AAO23018 standard;
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                                                                                                                                         Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ERSKTFTTWMVKDLQHHCQIHDAWSGLRHVVQLRAQEEFGQGEWSEWSPEAMGTPWTESR
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                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                  protein
                                                              to form 6. .174
                                                                                                                                                       Location/Qualifiers
                                            /label=
                                                                                             /note= "Dimer interface,
                                                                                                                          /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                           protein; 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61.4%;
                                                                                                                                                                                                                                  co-ordinate data; mutant;
"Dimer interface, a homodimer"
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                                             Disulphide_bond
                                                                           a homodimer
                                                                                                                        domain"
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L.9e-109;
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to form a homodimer"
179. .196
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                                               to form a homodimer" 284. .287
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226
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/note= "Double proline motif"
                              /note= "WSXWS motif"
                                                                             /note= "Dimer interface,
                                                                                                           /note=
                                                                                                                                         /note= "Dimer interface,
to form a homodimer"
                                                                                                                                                                                       /label= Trypt:
/note= "Forms
                                                                                                                                                                                                                                    261. .262
/note= "Dimer interface,
to form a homodimer"
                                                                                                                                                                                                                                                                                                                 /label= Tryptophan-arginine_ladder
/note= "Forms a left-handed_310 helix structure"
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co form a homodimer"
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note= "Forms a left-handed 310 helix structure"
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to form a homodimer"
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                                                                                                            "L7 loop"
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'Forms a left-handed 310 helix structure'
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                                                                             interact
                                                                                                                                                                                                                                                                                                                                                                                                                                 CC The invention relates to selecting or designing a compound that interacts content that interleukin-6 receptor (IL-6R) via assessing and obtaining the compound of the receptor and testing the compound and a topographic region of the receptor and testing the compound for its ability to compound and a tropographic region of the receptor and testing the compound for its ability to compound an activity associated with the receptor. Also disclosed is the crystal structure of the IL-6R alpha chain. The compounds of the compounds of the crystal structure of the greet receptor modulators and may be useful in the compounds of the crystal structure and treatment of diseases associated with signalling by IL-6R crystal as multiple myeloma, lymphoma, inflammation, rheumatoid arthritis, compounds the cancer, Castleman's disease, AIDS, mesangial proliferative compourtate cancer, Castleman's disease, AIDS, mesangial proliferative to the method provides enhanced stereochemical complementarity relative to the maturally occurring IL-6 receptor ligand as well as a rational basis for the development of ligands for specific therapeutic applications. The compound of the linear sequence is that of the human IL-6R crystal structure will facilitate a compound of the invention which contains a C192A compounds contains a c192A compounds contain sequence is not shown within the contain wild-type protein sequence (AAO23014)
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Page; 361pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Varghese JN,
Smith BJ;
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                                                                                                                                                                                                                                      RLLLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPEEPQLSCFRKSPLSNVVCEWGPRST
                                                                                                                                                                                                                                                                                                                                                                                                            325 AA;
   SPPAENEVSTPMQALTTNKDDDNIL
                                                ERSKTFTTWMVKDLQHHCVIHDAWSGLRHVVQLRAQEEFGQGEWSEWSPEAMGTPWTESR
                                                                                              SKFSKTQTFQGAGILQPDPPANITVTAVARNPRWLSVTWQDPHSWNSSFYRLRFELRYRA
                                                                                                                                                                                                                      RLLLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPEEPQLSCFRKSPLSNVVCEWGPRST
                                                                                                                                                                                                                                                                                   LAPRRCPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHWVLRKPAAGSHPSRWAGMGR
                                ERSKTFTTWMVKDLQHHCVIHDAWSGLRHVVQLRAQEEFGQGEWSEWSPEAMGTPWTESR
                                                                                                                                                        PSLITKAVLLVRKFQNSPAEDFQEPCQYSQESQKFSCQLAVPEGDSSFYIVSMCVASSVG
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3.1e-109;
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                                                                                                                                                                                                                                Query Match
Best Local S
Matches 323
                                                                                                                                                                                                                                                                                                         The invention relates to the production of human interleukin-6 receptor (IL-6R) protein in the fungus Pichia pastoris. The fungus was transformed with an expression vector (poIC9-A2OIL) containing a gene encoding an IL-6R protein having an immunoglobulin-like region and cytokine receptor region and spanning amino acids from Leu20-Ala323. The human IL-6R region was PCR amplified using the primers AAA70702-A70703. This sequence represents the recombinant IL-6R protein of the invention
                                                                                                                                                                                                                                                                                    Sequence 325
                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Page 6-8; 10pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                           Yeasts transformed with IL-6 receptor gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; interleukin-6 receptor; fungus; Pichia pastoris; PCR primer; expression vector; immunoglobulin-like region; cytokine receptor region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human interleukin 6 receptor protein.
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                                                                                                                                           RLLLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPEEPQLSCFRKSPLSNVVCEWGPRST
ERSKTFTTWMVKDLQHHCVIHDAWSGLRHVVQLRAQEEFGQGEWSEWSPEAMGTPWTESR
                                                                                                                             RLLLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPEEPQLSCFRKSPLSNVVCEWGPRST
                        SKFSKTQTFQGCGILQPDPPANITVTAVARNPRWLSVTWQDPHSWNSSFYRLRFELRYRA
                                       SKFSKTQTFQGGGILQPDPPANITVTAVARNPRWLSVTWQDPHSWNSSFYRLRFELRYRA
                                                                          PSLTTKAVLLVRKFQNSPAEDFQEPCQYSQESQKFSCQLAVPEGDSSFYIVSMCVASSVG
                                                                                         PSLTTKAVLLVRKFQNSPAEDFQEPCQYSQESQKFSCQLAVPEGDSSFYIVSMCVASSVG
                                                                                                                                                                               LAPRRCPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHWVLRKPAAGSHPSRWAEMGR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a method for the preparation of bovine interleukin 12 (BoIII12). BoIII12 consists of a heterodimer of p35 and p40 subunits. BoIII12 is produced by introducing into a host cell, recombinant vectors containing genes encoding the p35 and p40 subunits. This sequence represents the bovine II12 p35 subunit. Interleukin 12 is used for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 325 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Preparation of bovine interleukin 12 comprising using a vector containing the gene encoding it, useful for the prevention and treatment of chronic and opportunistic infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          prevention infections
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99.4%;
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Pred. No. 7.7e-109;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nephrotropic; osteopathic; antipsoriatic; interleukin-6 receptor alpha chain; cytokine; multiple myeloma; lymphoma; inflammation;
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to form a homodimer"
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190. .193
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93. .99
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/note= "pimer interface,
-~ form a homodimer"
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133. .138
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                                                "L4 loop"
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      The invention relates to selecting or designing a compound that interacts with the interleukin-6 receptor (IL-6R) via assessing and obtaining the stereochemical complementarity between the compound and a topographic region of the receptor and testing the compound for its abbility to modulate an activity associated with the receptor. Also disclosed is the crystal structure of the IL-6R alpha chain. The compounds of the invention act as cytokine receptor modulators and may be useful in the prevention and treatment of diseases associated with signalling by IL-6R such as multiple myeloma, lymphoma, inflammation, rheumacoid arthritis, prostate cancer, Castleman's disease, AIDS, mesangial proliferative glomerulonephritis, Kaposi's sarcoma, sepsis, osteoporosis and psoriasis.
                                                                                                                                                                                                                     Selecting or designing compound interacting with interleukin receptor, useful for treatment of e.g. AIDS, involves assessing and testing compound to modulate activity of receptor.
                                                                                                                                                                                                                                                                                                                   Varghese
Smith BJ;
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LUDWIG INST CANCER RES.
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227. .2
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/note= "Forms
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The method provides enhanced stereochemical complementarity relative to the naturally occurring IL-6 receptor ligand as well as a rational basis for the development of ligands for specific therapeutic applications. The information provided by the IL-6R crystal structure will facilitate a more accurate understanding of how the binding of a ligand leads to signal transduction. The current sequence is that of the human IL-6R alpha chain mutant protein of the invention which contains a W214N substitution. Note: The present sequence is not shown within the specification but was created by the indexer using the human IL-6R alpha chain wild-type protein sequence (AAO23014)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 325 AA;
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                                                                                                                                                                                  SKFSKTQTFQGCGILQPDPPANITVTAVARNPRWLSVTWQDPHSWNSSFYRLRFELRYRA 259
                                                                                                                                                                                                                                                               PSLTTKAVLLVRKFQNSPAEDFQEPCQYSQESQKFSCQLAVPEGDSSFYIVSMCVASSVG 199
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                                                                                                                                                                                                                                                                                                                                                                                                      LAPRRCPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHWVLRKPAAGSHPSRWAGMGR
                                                                                                                                                                                                                                                                                                                                                                                                                             LAPRRCPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHWVLRKPAAGSHPSRWAGMGR 79
                                                                                                                                                              SKFSKTQTFQGCGILQPDPPANITVTAVARNPRNLSVTWQDPHSWNSSFYRLRFELRYRA
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                                                                               ERSKTFTTWMVKDLQHHCVIHDAWSGLRHVVQLRAQEEFGQGEWSEWSPEAMGTPWTESR 300
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:
December 9, 2004, 08:55:07; Search time 47.8543 Seconds (without alignments)
1091.766 Million cell updates/sec

Title:
Sequence:
1 WS-09-462-416-7
Perfect score: 2861
Sequence:
1 MLAVGCALLAALLAAPGAAL......LILRSFKEFLQSSLRALRQM 543
Scoring table:
BLOSUM62
Gapop 10.0, Gapext 0.5
Searched:
283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters:
283416
Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

SUMMARIES

	150	161.5	166	167.5	167.5	171	178.5	21 180 6	198.5	226	301	17 306.5 10	310	330.5		374.5	396.5	465	10 471 16	476	557.5	.5	571.5 2	853	938.5 3	3 954.5 33	954.5 3	1 1918	Result Query	
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		prolactin receptor	interleukin-6 sign	membrane glycopro	æ	prolactin receptor		recept	interleukin 12B pr		•		ciliary neurotroph	interleukin-11 rec	interleukin-11 rec		interleukin-6 prec	9	interleukin-6 prec	9	interleukin 6 - p	-	interleukin-6 prec	6	interleukin-6 prec	interleukin-6 rece	interleukin-6 rec	in-6 re	Description	

ALIGNMENTS

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A;Gene: GDB:IL6R A;Cross-references: GDB:127966; OMIM:147880 A;Cross-references: GDB:127966; OMIM:147880 A;Cross-references: GDB:127966; OMIM:147880 A;Map position: 1921-1921 C;Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; immunogl C;Superfamily: ciliary neurotrophic factor receptor; dlycoprotein; transmembrane protein E;1-19/Domain: signal sequence #status predicted <sig- #status="" <mat="" f;20-468="" interleukin-6="" predicted="" product:="" receptor=""> F;20-468/Product: interleukin-6 receptor #status predicted <ext> F;20-363/Domain: extracellular #status predicted <ext> F;40-98/Domain: extracellular #status predicted <crs> F;121-309/Domain: cytokine receptor homology <crs> F;364-386/Domain: transmembrane #status predicted <tmm></tmm></crs></crs></ext></ext></sig->	A;Experimental source: hepatoma cell line HepG2 R;Novick, D.; Engelmann, H.; Wallach, D.; Rubinstein, M. J. Exp. Med. 170, 1409-1414, 1989 A;Title: Soluble cytokine receptors are present in normal human urine. A;Reference number: A61459; MUID:90010793; PMID:2529343 A;Accession: A61459 A;Molecule type: protein A;Residues: 20-49 <nov> C;Comment: Through this receptor, interleukin-6 induces proliferation, activation, and di C;Comment: This growth factor receptor does not have a tyrosine kinase domain. C;Genetics: This growth factor receptor does not have a tyrosine kinase domain.</nov>	A;Title: Molecular structure of interleukin 6 receptor. A;Reference number: JU0080 A;Reference number: JU0080 A;Reference number: JU0080 A;Accession: JU0080 A;Molecule type: mRNA A;Residues: 1-468 <xa2> A;Celemitink, H; Stoyan, T; Lenz, D.; Schmitz, H.; Hirano, T.; Kishimoto, T.; Heinrich, Biochem. J. 277, 659-664, 1991 Biochem. J. 277, 659-664, 1991 A;Title: Structural and functional studies on the human hepatic interleukin-6 receptor. N A;Reference number: S17468; MUID:91336983; PMID:1872801 A;Recession: S17468 A;Residues: 1-468 <sch> A;Residues: 1-468 <sch> A;Cross-references: EMBL:X58298; NID:932580; PIDN:CAA41231.1; PID:932581 A;Cross-references: EMBL:X58298; NID:932580; PIDN:CAA41231.1; PID:932581</sch></sch></xa2>	RESULT 1 A41242 interleukin-6 receptor precursor - human N;Contains: interleukin-6 receptor, soluble form C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 27-Mar-1992 #sequence revision 02-Dec-1994 #text_change 09-Jul-2004 C;Accession: A41242; JU0000; S17468; A61459; S14621 R;Yamasaki, K.; Taga, T.; Hirata, Y.; Yawata, H.; Kawanishi, Y.; Seed, B.; Taniguchi, T.; Science 241, 825-828, 1988 A;Title: Cloning and expression of the human interleukin-6 (BSF-2/IFNbeta 2) receptor. A;Reference number: A41242; MUID:88305347; PMID:3136546 A;Accession: A41242 A;Molecule type: mRNA A;Residues: 1-468 «YAM» A;Cross-references: UNIPROT:P08887; GB:M20566; NID:g33845; PIDN:CAA31312.1; PID:g33846 R;Yamasaki, K.; Taga, T.; Hirata, Y.; Yawata, H.; Kawanishi, Y.; Seed, B.; Taniguchi, T.; Brock Accession: Accession Acces

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A;Title: Functional murine interleukin 6 receptor with the intracisternal a particle gen A;Reference number: JL0144; MUID:90278354; PMID:2112585
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C;Specites: Mus musculus (house mouse)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C;Accession: JL0144
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F;47-96/Disulfide bonds: #status predicted
F;55,93,221,245,350/Binding site: carbohydrate (Asn) (covalent) #status predicted
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CFRKSPLSNVVCEWGPRSTPSLTTKAVLLVRKFQNSPAE-DFQEPCQYSQESQKFSCQLA 179
                                                                                                                                               MLTVĠĊTLLVĀLLĀĀPAVĀLVLGSĊRĀLEVĀNGTVTSLÞGATVTLICÞGKEAAGNVTIHW
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96.5%;
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A;Molecule type: mRNA
A;Residues: 1-373; 'R',375-460 <FIO>
A;Cross-references: EMBL:X53802; NID:g52692; PIDN:CAA37810.1; PID:g52693
C;Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; immunog]
C;Keywords: cytokine receptor; transmembrane protein
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-460/Product: interleukin-6 receptor #status predicted <MAT>
F;40-94/Domain: immunoglobulin homology <IMM>
F;117-016/Domain: cytokine receptor homology <CRS>
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(;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C;Accession: JL0145; S14543
R;Sugita, T.; Totsuka, T.; Saito, M.; Yamasaki, K.; Taga, T.; Hirano, T.; Kishimoto,
J. Exp. Med. 171, 2001-2009, 1990
A;Title: Functional murine interleukin 6 receptor with the intracisternal a particle
A;Reference number: JL0144; MUID:90278354; pMID:2112585
A;Accession: JL0145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        180 VPEGDSSFYIVSMCVASSVGSKFSKTQTFQGCGILQPDPPANITVTAVARNPRWLSVTWQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        117
                                                                                                                                                                                                                                                                                                                                                                                                         h 33.4%; Score 954.5; DB 2;
Similarity 50.1%; Pred. No. 1.6e-58;
88; Conservative 52; Mismatches 122;
          ILEGDKVYHIVSLCVANSVGSKSSHNEAFHSLKWVQPDPPANLVVSAIPGRPRWLKVSWQ
                                      CFRKSPLSNVVCEWGPRSTPSLTTKAVLLVRKFQNSPAE-DFQEPCQYSQESQKFSCQLA 179
                                                                                                                                                                                                                                    VLRKPAAGSHESRWAGMGRRLLLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPEEEPQLS 120
                                                                                                                                                                                                          VY----SGSQNREWTTTGNTLVLRDVQLSDTGDYLCSLNDHLVGTVPLLVDVPPEEPKLS
                                                                                                                                                                                                                                                                                                         MLTVGCTLLVALLAAPAVALVLGSCRALEVANGTVTSLPGATVTLICPGKEAAGNVTIHW
                                                                                                                                                                                                                                                                                                                                      MLAVGCALLAALLAADGAALAPRRCPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHW
                                                                                                      CFRKNPLVNAICEWRPSSTPSPTTKAVLFAKKINTTNGKSDFQVPCQYSQQLKSFSCQVE 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QGEWSEWSPEAMGTPW-TESRSPPAENEVSTPMQALTTNKDDDNILFRDSANATSLPVEF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --LAPVQESSSMSLP
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PID: 949726

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236 239

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A;Accession: A;Acc
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A;Experimental source: fibroblast
R;May, L.T.; Helfgott, D.C.; Sehgal, P.B.
Proc. Natl. Acad. Sci. U.S.A. 83, 8957-8961, 1986
Proc. Natl. Acad. Sci. U.S.A. 83, 8957-8961, 1986
A;Title: Anti-beta-interferon antibodies inhibit the increased expression
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                                                                                           A; Molecule type: mRNA
A; Residues: 1-212 < MAY >
                                                                                                                                                                                 A; Reference number: A25921;
A; Accession: A25921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA; mRNA
A; Residues: 1-212 <HAE>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-212 <HIR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Complementary DNA for a novel human interleukin (BSF-2) that induces A;Reference number: A93387; MUID:87065033; PMID:3491322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1, T.; Kishimoto, T
Nature 324, 73-76,
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R;Hirano, T.; Yasukawa, K.; Harada, H.; Taga, T.; Watanabe, Y.; Matsuda,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-212 <ZIL>
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C;Accession: A32648; A25692; A26966; A33515; A25801; A25921; I52193; I56003; A27601; B2:
C;Accession: A32648; A25692; A26966; A33515; A25801; A25921; I52193; I56003; A27601; B2:
R;Yasukawa, K.; Hirano, T.; Watanabe, Y.; Muratani, K.; Matsuda, T.; Nakai, S.; Kishimot
EMBO J. 6, 2939-2945, 1987
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    Cross-references: GB:M14584; Wong, G.G.; Witek-Giannotti,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Residues: 1-212 <YAS>
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2529-2537, 1986
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ames: B-cell differentiation factor; B-cell hybridoma growth factor;
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1986
    NID:g184628; PIDN:AAA52728.1; PID:g306910 J.; Hewick, R.M.; Clark, S.C.; Ogawa, M.
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A;Experimental source: FS-4 fibr
A;Note: sequence extracted from
A;Note: this 23-25K form contain
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A;Accession: A29085
A;Molecule type: protein
A;Residues: 29-42 <a href="Array of the Indian Array of Indian Indian
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A;Residues: 30-43 <YAM>
R;Hirano, T.; Taga, T.; Yasukawa, K.; Nakajima, K.; Nakano,
Proc. Natl. Acad. Sci. U.S.A. 84, 228-231, 1987
A;Title: Human beta-cell differentiation factor defined by
A;Reference number: A29085; MUID:87092370; PMID:3491991
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A;Residues: 30-56; XXX,59-61,'X',63 <VA2>
R;Yamamoto, R.; Lin, L.S.; Lowe, R.; Warren, M.K.; White, T.J.
J. Immunol. 144, 1808-1816, 1990
A;Title: The human lung fibroblast cell line, MRC-5, produces multiple factors involved A;Reference number: A60400; MUID:90171574; PMID:2307841
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                                                                                                                                                                                                                                                                                                 A;Molecule type: protein
A;Residues: 30-37,'X',39-40 <MAY2>
A;Experimental source: FS-4 fibroblasts
A;Note: sequence extracted from NCBI backbone
A;Note: this 28-30K form contained both N-linked and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;May, L.T.; Shaw, J.E.; Khanna, A.K.; Zabriskie, Cytokine 3, 204-211, 1991
A;Title: Marked cell-type-specific differences in A;Reference number: A48419; MUID:91355644; PMID:18
A;Accession: A48419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Accession: A61462
A;Molecule type: protein
A;Residues: 28-48 <MIN>
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J. Mol. Cell. Immunol. 4, 203-212, 1989
A,Title: Interleukin 6 is the principal cytolytic T lymphocyte differentiation factor for A,Reference number: A61462; MUID:90121567; PMID:2610854
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A; Residues: 28-51, 'X', 53-57, 'X', 59, 'X', 61 < VAN1>
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A; Title: Interleukin 6: Identification as a hematopoietic A; Reference number: IS2193; MUID:89193317; PMID:3266463
                                                                                                                                                          A;Accession: C48419
A;Molecule type: protein
A;Residues: 28-40 <MAY3>
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fibroblasts
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from NCBI backbone (NCBIP:63787)
ntained O-linked but not N-linked
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of human fibroblast PMID:1648338
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De Ley, M.;
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R;Baumann, M.; Baumann, H.; Fey, G.H.
J. Biol. Chem. 265, 19853-19862, 1990
A;Title: Molecular cloning, characterization and functional expression of the rat liver A;Reference number: A37986; MUID:91060602; PMID:2174054
A;Recession: A37986
A;Rolecule type: mRNA
A;Residues: 1-462 cBAU>
A;Cross-references: UNIPROT:P22273; GB:M58587; GB:J05668; NID:g204921; PIDN:AAA41431.1;
C;Comment: After binding IL-6, this chain associates with a 130K glycoprotein that is est; Comment: actor phenomenous phic factor receptor; cytokine receptor c;Keywords: acute phase; cytokine receptor; transmembrane protein
F;1-19/Domain: signal sequence #status predicted <SIG>
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A;Contents: annotation; modified sites in recombinant protein from CHO cells
R;Clogston, C.L.; Boone, T.C.; Crandall, C.; Mendiaz, E.A.; Lu, H.S.
Arch. Biochem. Biophys. 272, 144-151, 1989
A;Title: Disulfide structures of human interleukin-6 are similar to those of human granu
A;Reference number: S04981, MUID:9286115; PMID:2472117
A;Contents: annotation; disulfide bonds in recombinant protein
A;Reference number: S04981, MUID:9427014; PMID:9472117
A;Contents: annotation; disulfide bonds in recombinant protein
A;Reference number: S146-5154, 1994
A;Title: Roles of disulfide bonds in recombinant human interleukin 6 conformation.
A;Reference number: A54253; MUID:94227044; PMID:9172889
A;Contents: annotation; lability and functional significance of each disulfide bond
C;Comment: Produced by both lymphoid and nonlymphoid tissue in response to growth factor lobulin secretion). It therefore appears to function as an autoregulator of cell growth C;Comment: This protein plays a regulatory role in various host defense mechanisms and e
                                                                                                                                                                                                                                                                                                                                                                                                       interleukin-6 receptor precursor - rat
N;Alternate names: IL-6 receptor
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
C;Accession: A37986
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A37986
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A;Introns: 7/1, 70/3; 108/3; 157/3

C;Superfamily: interleukin-6

C;Keywords: Castleman's disease; cytokine; extracellular protein; glycoprotein; ;

F;1-27/Domain: signal sequence #status predicted <SIGs

F;28-212/Product: interleukin-6, long form #status experimental <MATLs

F;30-212/Product: interleukin-6, short form #status experimental <MATSs

F;12-78,101-111/Disulfide bonds: #status experimental

F;73/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental

F;166/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental

F;172/Binding site: carbohydrate (Asn) (covalent) #status experimental
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em. 115, 345-350, 1994
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Pred. No. 7.2
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A; Molecule type: mRNA
A; Residues: 1-208 <SWI>
A; Cross-references: UNIPI
C; Genetics:
A; Gene: II-6
C; Superfamily: interleuk:
C; Keywords: cytokine; gro
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A;Accession: T09216
A;Status: preliminary; tran
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               interleukin-6 precursor - horse
C;Species: Equus caballus (domestic horse)
C;Date: 11-Jun-1999 #sequence_revision 11-
C;Accession: T09216
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T09216
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Best Local :
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                                                                                                                                                                                                                                                         cytokine; growth
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                                                        SSKEALAENNLNLPKMAEKDGCFQSGFNEETCLVKIITGLLEFEVYLEYLQNRFESSEEQ
                                                                                                                                       ATSLPVEFMPVPPGEDSKDVAAPHRQPLTSSERIDKQIRYILDGISALRKETCNKSNMCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RAQEEFGQGEWSEWSPEAMGTPW-TESRSPPAENEVSTPMQALTTNKDDDNILFRDSANA
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ARAVQMSTKVLIQFLQKKAKNLDAITTPDPTTNASLLTKLQAQNQWLQDMTTHLILRSFK
                                  NSKEVLAENNLNLPKMAEKDGCFQSGFNQETCLMKITTGLSEFQIYLEYLQNEFKGEKEN
                                                                                                          ATAFPT---PLPLGEDETTSNGP---LLTTADKTKQHIKYILGKISALKNEMCNNFSKCE
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                                                                                                                                                                                   Conservative
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                                                                                                                                                                                 20.0%; Score 571.5; DB 2
58.5%; Pred. No. 1.9e-32;
ative 32; Mismatches 41
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Pred. No. 1.7e-51;
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prointerleukin (
C;Species: Sus s
C;Date: 21-Feb-1
                                                                                                                                                                                                                                              R;Mathialagan, N.; Bixby, J.; Roberts, M.R.
Mol. Reprod. Dev. 32, 324-330, 1992
A;Title: Expression of interleukin-6 in porcine, ovine,
A;Reference number: I46590; MUID:92360284; PMID:1497880
                                                                                                                                                                                                                                                                                                                        interleukin 6 - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Accession: 146621
R;Richards, C.; Saklatva, J.
Cytokine 3, 269-276, 1991
Cytokine 3, 269-276, 1991
A;Title: Molecular Cloning and Sequence of Porcine Interleukin 6 cDNA and A;Reference number: 146621; MUID:91338547; PMID:1873476
A;Accession: 146621
                                                                                                                                                                               A;Accession: I46590
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-212 <MAT>
                                                                                                                                                                                                                                                                                                                 C;Date: 21-Feb-1997
C;Accession: I46590
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C;Superfamily: interleukin-6
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A; Residues: 1-212 < RIC>
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                                                                                                                                                                A;Cross_references: UNIPROT:P26893; GB:M80258; NID:g164514; PIDN:AAC27127.1; PID:g16451
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;Species: Sus scrofa domestica (domestic pig)
;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
                                                                                                                  ;Superfamily: interleukin-6
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Best Local Similarity
Matches 112; Conserv
                                                                     Query Match
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                                                                     Similarity
ATSLPVEFMPVPPGEDSKDVAAPHRQPLTSSERIDKQIRYILDGISALRKETCNKSNMCE 410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SFKEFLOSSLRALROM 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KGNVEAVQISTKALIQTLRQKGKNPDKATTPNPTTNAGLLDKLQSQNEWMKNTKIILILR
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                                                   19.5%;
ilarity 57.5%;
Conservative 3
                                                    32;
                                                                  Score 557.5; DB 2; Pred. No. 1.8e-31;
                                                    Mismatches
                                                    47;
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C;Species: Bos primigenius taurus (cattle)
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A56610; S22162
R;Droogmans, L; Cludts, I; Cleuter, Y.; Kettmann, R.; Burny, A.
DNA Seq. 2, 411-413, 1992
A;Title: Nucleotide sequence of bovine interleukin-6 cDNA.
A;Reference number: A56610; MUID:93076003; PMID:1446077
A;Accession: A56610
A;Status: preliminary
A;Status: preliminary
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A;Title: Molecular cloning and characterization of a cDNA encoding A;Reference number: 146084; MUID:94052249; PMID:8234373
A;Accession: 140084
A;Residues: 1-208 <DRO>
A;Residues: 1-208 <DRO>
A;Cross-references: UNIPROT:P26892; EMBL:X57317; NID:g2193; PIDN:CAA40572.1;
A;Experimental source: BLV induced B cell-lymphosarcoma
A;Experimental source: Grom NCBI backbone (NCBIP:118917)
C;Superfamily: interleukin-6
C;Keywords: cytokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:P41683; GB:L16914; NID:g438519; PIDN:AAA16620.1; PID:g438520 C;Superfamily: interleukin-6
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C;Species: Felis silvestris catus (domestic cat)
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A; Residues: 1-207 < BRA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                      interleukin-6 precursor - bovine
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RESULT 11
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                                            C;Accession: A34247

R;Northemann, W.; Braciak, T.A.; Hattori, M.; Lee, F.; Fey, G.H.
J. Biol. Chem. 264, 16072-16082, 1989

A;Title: Structure of the rat interleukin 6 gene and its expression
A;Reference number: A34247; MUID:89380206; PMID:2789217
A;Accession: A34247
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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-211 <NOF
                                                                                                                                          C;Species: Rattus norvegicus (Norway rat)
C;Date: 15-Jun-1990 #sequence_revision 15-Jun-1990 #text_change 09-Jul-2004
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A;Residues: 1-208 <EBR>
A;Cross_references: UNIPROT:P29455; EMBL:X68723
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larity 50.5%; Pred. No. 4.5e-25;
Conservative 34; Mismatches 52;
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A;Cross-references: UNIPROT:P20607; GB:M26744; NID:g204915; PIDN:AAA77659.1; PID:g204916 C;Superfamily: interleukin-6 C;Keywords: cytokine; growth factor; immunoregulation; lymphokine; macrophage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1990 #sequence revision 30-Jun-1990 #text change 09-Jul-2004
C;Accession: A30531; A27610; A30571; S01323; S12103; E34047; A26662; A40486;
R;Tanabe, O.; Akira, S.; Kamiya, T.; Wong, G.G.; Hirano, T.; Kishimoto, T.
R;Tanabe, O.; Akira, S.; Kamiya, T.; Wong, G.G.; Hirano, T.; Kishimoto, T.
A;Title: Genomic structure of the murine IL-6 gene. High degree conservation A;Reference number: A30531; MUID:89035525; PMID:3263439
A;Accession: A30531
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R;Simpson, R.J.; Moritz, R.L.; Rubira, M.R.; Van Snick, J.
Bur. J. Biochem. 176, 187-197, 1988
A;Title: Murine hybridoma/plasmacytoma growth factor. Complete amino-acid sequence and A;Reference number: S01323; MUID:88329059; PMID:3262059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:X06203; NID:g52701; PIDN:CAA29560.1; PID:g52702 R;Mock, B.A.; Nordan, R.P.; Justice, M.J.; Kozak, C.; Jenkins, N.A.; Cop A;Timunol. 142, 1372-1376, 1989 A;Title: The murine Il-6 gene maps to the proximal region of chromosome A;Reference number: A30571; MUID:89124383; PMID:2563387 A;Accession: A30571
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                                                                                     Nucleic Acids Res. 18, 6455, 1990
A;Title: Cloning and sequence analysis of t
A;Reference number: S12103; MUID:91057159;
A;Accession: S12103
                                                                                                                                                                          A;Molecule type: protein
A;Residues: 25-166,'X',188-211 <SIM>
A;Rosidues: 25-166,'X',188-211 is inconsistent with that
A;Note: the sequence from Fig. 11 is inconsistent with that
R;Grenett, H.E.; Fuentes, N.L.; Fuller, G.M.
Nucleic Acids Res. 18, 6455, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-211 < VAN>
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A; Cross-references: EMBL: X54542; NID: g52727;
                        A; Molecule type: mRNA
A; Residues: 1-211 <GRE>
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A; Residues: 5-211 < MOC>
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Similarity 39.4%;
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; Pred. No. 2.5e-20;
53; Mismatches 59;
                                                                                                                          the cDNA for murine; PMID:2243807
            PIDN:CAA38411.1; PID:g52728
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A;Map position: 5
A;Introns: 7/1; 68/3; 106/3; 156/3
C;Superfamily: interleukin-6
C;Superfamily: interleukin-6
C;Keywords: Castleman's disease; cytokine; growth factor; immunoregulation;
C;Keywords: Castleman's disease; cytokine; growth factor; immunoregulation;
F;1-24/Domain: signal sequence #status predicted <SIG>
F;1-24/Domain: signal sequence #status predicted <SIG>
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A;Residues: 77-98 <SHA>
R;Blankenstein, T.; Qin, Z.; Li, W.; Diamantstein, T.
J. Exp. Med. 171, 965-970, 1990
A;Title: DNA rearrangement and constitutive expression capreference number: S10241; MUID:90171860; PMID:2106569
A;Accession: S10241
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A;Title: The myeloid blood cell differentiation-inducing protein MGI-2A is in A;Reference number: A60799; MUID:89062753; PMID:3264198
A;Accession: A60799
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A; Residues: 25-39; X', 41-42, 'X', 44-45 < VSN>
A; Residues: 25-39; X', 41-42, 'X', 44-45 < VSN>
R; Chiu, C. P.; Moulds, C.; Coffman, R.L.; Rennick, D.; Lee, F.
R; Chiu, C. P.; Moulds, C.; Coffman, R.L.; Rennick, D.; Lee, F.
Proc. Natl. Acad. Sci. U.S.A. 85, 7099-7103, 1988
A; Title: Multiple biological activities are expressed by a mouse
A; Reference number: A40486; MUID:89017145; PMID:3262872
A; Accession: A40486
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A;Molecule type: protein
A;Residues: 38-60;75,'X',77-79;176-203
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A; Residues: 1-6 <BLA>
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A; Title: Purification and NH2-terminal amino acid sequence
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A; Residues: 66-69'X', 71-75; 78-94; 128-148 < JA5>
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Matches 76
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EFLQSSLRALRQ 542
                                                                         ARVLQRDTETLIHIFNQEVKDLHKIVLPTPISNALLTDKLESQKEWLRTKTIQFILKSLE 198
                                                                                                                    ARAVQMSTKVLIQFLQKKAKNLDAITTPDPTTNASLLTKLQAQNQWLQDMTTHLILRSFK
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interleukin-11 receptor alpha chain - human C;Species: Homo sapiens (man) C;Date: 29-May-1998 #sequence revision 29-Mc;Accession: I37891; G01970; G01971
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A;Gene: Bt12/IL11
C;Superfamily: ciliary neurotrophic factor receptor;
C;Keywords: cytokine receptor
E;120-310/Domain: cytokine receptor homology <CRS>
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A;Title: et12, a novel putative type-1 cytokine receptor expressed during mouse embryoger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I48343; S51619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-432 <HIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: Cloning of a murine IL-11 receptor alpha-chain; A;Reference number: S51619; MUID:95045367; PMID:7957045 A;Accession: S51619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:Q64385; EMBL:X74953; NID:g673437; PIDN:CAA52908.1; PID:g6734: R;Hilton, D.J.; Hilton, A.A.; Raicevic, A.; Rakar, S.; Harrison-Smith, M.; Gough, N.M.; EMBO J. 13, 4765-4775, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-references: EMBL: U14412; NID: g576454; PIDN: AAA53248.1;
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A; Accession: I48343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LAVGCALLAALLAAPGAAL--APRRCPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVH
                                                                                                                                                                   MVXDLQHHCVIHDAWSGLRHVVQLRAQEEFGQGEWSEWSPEAMGTPWTESRSPPAENEVS
                                                                                                                                                                                                                                             LOSILREDEPOGLRVESVEGYERRLHASWTYEASWRROPHFLLKFRLOYREAOHEAWST-
                                                                                                                                                                                                                                                                                                                                                                       STGPWPC----PQDPLEASRCVVHGAEFWSEYRINVTEVNPLGA-----STCLLDVR
                                                                                                                                                                                                                                                                                                                                                                                                                                ----PCQYSQESQKFSCQLAVPEGDS--SFYIVSMCVASSVGSKFSKTQTFQGC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VHLLVDVPPEEPQLSCFRKSPLSNVVCEWGPRSTPSLTTKAVLLVRKFQNSPAEDFQE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WVLRKPAAGSHPSRW-------AGMGRRLLLRSVQLHDSGNYSCYRA-GRPAGT 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MSSSCSGLTRVLVAVATALVSSSSPCPQAWGPPGVQYGQPGRPVMLCCPGV--
                                                      TPMQALTINKDDDNILFRDSANATSLPVEFMPVPPGEDSKDVAAPHRQPL 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VTLKLGFPPARPEVSC-QAVDYENFSCTWSPGQVSGLPTRYLTSYRKKTLPGAESQRESP 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----SAGT-PVSWFRDGDSRLLQGPDSGLGHRLVLAQVDSPDEGTYVCQTLDGVSGGM 104
                                                                                                                                                                                                                                                                                                      --GILQPDPPANITVTAVARNPRWLSVTWQDPHSW-NSSFYRLRFELRYRAERSKTFTTW
-PDWSQGHGQQLEAVVAQEDSPAPARP-SLQPDPRPLD-
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29-May-1998 #text_change

09-Jul-2004

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ciliary neurotrophic factor receptor alpha chain - rat C;Species: Rattus norvegicus (Norway rat) C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004 C;Accession: I58141; A47387 R;Ip, N.Y.; McClain, J.; Barrezueta, N.X.; Aldrich, T.H.; Pan, L.; Li, Y.; Wiegand, Neuron 10, 89-102, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Cherel, M.; Sorel, M.; Lebeau, B.; Dubois, S.; Moreau, J.F. Blood 86, 2534-2540, 1995
A;Title: Molecular cloning of two isoforms of a receptor for A;Reference number: 137891; MUID:95399754; PMID:7670098
A;Accession: 137891
Neuron 10, 89-102, 1993
A;Title: The alpha component of the CNTF receptor is required for
A:Reference number: IS8141; MUID:93152175; PMID:8381290
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A; Residues: 1-422 < RES >
A; Cross-references: UNI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Reference number: G08959
A; Accession: G01970
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C; Genetics:
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A; Residues: 1-422 < VA2>
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A;Status: preliminary; translated from GB/EMBL/DDBJ
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A; Residues: 1-422 < VAN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ITVTAVARNPRWLSVTWQDPHSWN-SSFYRLRFELRYRAERSKTFTTWMVKDLQHHCVIH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VPPEEPQLSCFRKSPLSNVVCEWGPRSTPSLTT-----KAVLLVRKFQNSPAEDFQE 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WFRDGEPKLLQGPD-----SGLGHELVLAQADSTDEGTYICQTLDGALGGTVTLQLG 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PC----PQDPLGAARCVVHGAEFWSQYRINVTEVNPLGAS-TRLLDVSLQSILRPDPPQG
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                                                                                                                                                                                                                                                                                                                              354
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C;Superfamily: ciliary neurotrophic factor r C;Keywords: growth factor receptor F;2-99/Domain: immunoglobulin homology <IMM>F;114-294/Domain: cytokine receptor homology

receptor homology

<CRS:

A; Cross-references: UNIPROT: P51641; C; Superfamily: ciliary neurotrophic

EMBL: Z48168; NID: g971417;

factor receptor;

cytokine

PIDN:CAA88184.1; PID:g3063; receptor homology; immunogl

A; Molecule type: mRNA A; Residues: 1-362 < HE

1-362 <HEL>

A; Status: preliminary; nucleic acid sequence

not

A; Accession: S60614

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A;Cross-references: UNIPROT:Q08406; GB:S54212; NID:g265055; PIDN:AAB25290.1; PID:g265056
R;Clatterbuck, R.E.; Price, D.L.; Koliatsos, V.E.
Proc. Natl. Acad. Sci. U.S.A. 90, 2222-2226, 1993
A;Title: Ciliary neurotrophic factor prevents retrograde neuronal death in the adult cent A;Reference number: A47387; MUID:93211934; PMID:8460125
A;Reference number: MA7387; MUID:93211934; PMID:8460125
A;Rocession: A47387; MUID:93211934; PMID:8460125
A;Rocession: Preliminary
A;Rolecule type: mRNA
A;Residues: preliminary
A;Rolecule type: mRNA
A;Residues: 185-260, 'D', 262-277 < CLA>
A;Roserreferences: GB:S57711; NID:g299331; PIDN:AAB25918.1; PID:g299332
A;Cross-references: GB:S57711; NID:g299331; PIDN:AAB25918.1; PID:g299332
A;Rote: sequence extracted from NCBI backbone (NCBIN:128471, NCBIP:128472)
C;Superiamily: ciliary neurotrophic factor receptor; Cytokine receptor homology; immunogl
C;Keywords: growth factor receptor
F;33-91/Domain: immunoglobulin homology < IMM'
F;116-296/Domain: cytokine receptor homology < CRS>
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A;Status: preliminary;
A;Molecule type: mRNA
A;Residues: 1-372 <IPN
Development 121, 2681-2693, 1995
A; Title: Analysis of function and expression of the chick A; Reference number: S60614; MUID:95401882; PMID:7671828
                                                                                                                   growth promoting activity receptor alpha precursor - chicken C;Species: Gallus gallus (chicken) C;Date: 27-Apr-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
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                                                                          C;Accession: S60614
R;Heller, S.; Finn, T.P.; Huber, J.; Nishi, R.; Geissen, M.; Pueschel, A.W.; Rohrer,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1-372 <IPN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LFSTIKYKVSISVSNALGHN-TTAITFDEFTIVKPDPPENVVARPVPSNPRRLEVTWQTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GFYCSWHLSAPTYIPNTFNVTVLHGSKMMVCEKDPA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NVVCEW----GPRSTPSLTTKAVLLVRKF----QNSPAEDFQEPCQYSQESQKFSCQLAVPE
                                                                                                                                                                                                                                                                                                                                                                                                    AAKDN-EIGTWSDWSVAAHATPWTEE----PRHLTTEAQAPET
                                                                                                                                                                                                                                                                                                                                                                                                                                                  RAQEEFGQGEWSEWSPEAMGTPWTESRSPPAENEVSTPMQALTINKDDDNILFRDSANAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STWPDPESFPLKFFLRYRP-----LILDQWQHVELSNGTAHTITDAYAGKEYIIQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GDSSF-YIVSMCVASSVGSKFSKTQTFQGCGILQPDPPANITVTAVARNPRWLSVTWQDP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PSRWAGMGRRLLLRSVQLHDSGNYSCYR--AGRPAGTVHLLVDVPPEEPQLSCFRKSPLS 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AVLAAAAAAVYTOKHSPOE-APHVOYERLGTDVTLPC-GTASWD-AAVTWRVN----GTD
                                                                                                                                                                                                                                                                                                      STTSSLAPPPTTKICDPGE
                                                                                                                                                                                                                                                                                                                                                      SLPVEFMPVP----
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Pred. No. 5.3e-14;
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                                 GPA
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                            receptor
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                                 (GPARalpha)
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N;Alternate names: CNTF receptor
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
C;Accession: A40854; A56526
R;Davis, S.; Aldrich, T.H.; Valenzuela, D.M.; Wong, V.; Furth, M.E.; Squinto Science 253, 59-63, 1991
A;Title: The receptor for ciliary neurotrophic factor.
A;Reference number: A40854; MUID:91289158; PMID:1648265
A;Accession: A40854
                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: DNA, A;Molecule type: DNA, A;Residues: 1-346, S', 348-372 <VAL>
A;Residues: 1-346, S', 348-372 <VAL>
A;Cross-references: GB:L38025; NID:9608654; PIDN:AAA91337.1; PID:9608656
C;Comment: The CNTF receptor is attached to the membrane by a glycosylphosphatidylinosic C;Comment: The CNTF receptor sequence appears to contain several PEST regions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:P26992; GB:M73238
R;Valenzuela, D.M.; Rojas, E.; Le Beau, M.M.; Espinosa III, R.; Brannan, Genomics 25, 157-163, 1995
A;Title: Genomic organization and chromosomal localization of the human a A;Reference number: A56526; MUID:95293367; PMID:7774913
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                                                            Local Similarity
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  CALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHWVLRKP 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LDQWQHVELSDGTSHTITDAYAGKEYIIQVAAKDN-DIGTWSDWSVAVHATPWTEE----
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                                            Conservative
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                                        44;
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                                                                Score 301;
Pred. No. 2
                                          ced. No. 2.2e-13;
Mismatches 150;
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                                                                                  DB 1;
                                                                                Length 372,
                                          Indels
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                                                                                                                                                                                                               N; Alternate names:
C; Species: Homo san
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A; Gene: sIL-6R
C; Superfamily: (
C; Keywords: cyto
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153394
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A;Molecule type: mRNA
A;Residues: 1-53 <RES>
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Eur. J. Immunol. 24, 1945-1948, 1994
A;Title: Soluble interleukin-6 receptors released from T cell
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                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Soluble interleukin-6 receptor - human (fragment)
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                                                                                                                                                                                                                                                                                                                                                                                                          C; Accession:
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                                                                                                                                           ;Superfamily: ciliary neurotrophic factor receptor; ;Keywords: cytokine receptor
                                                                        Matches
                                                                                      Query Match
Best Local Similarity
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                     TPWTESRSPPAENEVSTPMQALTTNKDDDNILFRDSANATSLP 355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LAVPEGDSSF-YIVSMCVASSVGSKFSKTQTFQGCGILQPDPPANITVTAVARNPRWLSV 236
TPWTESRSPPAENEVSTPMQALTTNKDDDNILFRDSANATSLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YIIQVAAKDN-EIGTWSDWSVAAHATPWTEE----PRHLTTEAQAAET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TWODPHSW-NSSFYRLRFELRYRAERSKTFTTWMVKDLQHHC-----VIHDAWSGLR 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IRYMHLFSTIKYKVSISVSNALGHN-ATAITFDEFTIVKPDPPENVVARPVPSNPRRLEV
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                                                                      Conservative
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                                                                                      7.9%;
                                                                      <u>.</u>
                                                                      Score 226; DB 2;
Pred. No. 2.6e-09;
0; Mismatches 0;
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                                                                        Indels
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                                                                                                                                                                receptor homology;
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                                                                      Gaps
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i, G.; Perussia, B.
J. Immunol. 146, 3074-3081, 1991
A;Title: Cloning of cDNA for natural killer cell stimulatory factor, a heterodimeric A;Reference number: A38957; MUID:91201875; PMID:1673147
A;Accession: A38957
A;Molecule type: mRNA
A;Residues: 1-328 <WOL>
                                                                                                                                                                                                                                                             C;Species: Homo sapiens (man)
C;Date: 18-Aug-1995 #sequence revision 18-Aug-1995 #text_change 09-Jul-2004
C;Accession: A38957; B39359; S21688; B36055
R;Wolf, S.F.; Temple, P.A.; Kobayashi, M.; Young, D.; Dicig, M.; Lowe, L.;
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cyto

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A38957

cytotoxic lymphocyte maturation factor 40K chain; natural killer

cel1

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A;Experimental source: lymphoblastoid cell line NC-37
C;Genetics:
A;Genetics:

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        prolactin receptor precursor - chi
C;Species: Gallus gallus (chicken)
C;Date: 30-Sep-1993 #sequence_revi
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A;Roseidues: 23-28,46-59;74-80,'X',94-130;161-169,'X',171-180;213-235;240-250;289-299,'X'
A;Residues: 33-28,46-59;74-80,'X',94-130;161-169,'X',171-180;213-235;240-250;289-299,'X'
A;Resperimental source: lymphoblastoid cell line NC-37
R;Stern, A.S.; Podlaski, F.J.; Hulmes, J.D.; Pan, Y.C.E.; Quinn, P.M.; Wolitzky, A.G.; F
Proc. Natl. Acad. Sci. U.S.A. 87, 6808-6812, 1990
A;Title: Purification to homogeneity and partial characterization of cytotoxic lymphocyt
A;Reference number: A36055; MUID:90370873; PMID:2204066
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A;Reference number: S21688; MUID:92198015; PMID:1347984
A;Accession: S21688
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R;Gubler, U.; Chua, A.O.; Schoenhaut, D.S.; Dwyer, C.M.; McComas, W.; Motyka, Proc. Natl. Acad. Sci. U.S.A. 88, 4143-4147, 1991
A;Title: Coexpression of two distinct genes is required to generate secreted be A;Reference number: A39359; MUID:91239523; PMID:1674604
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A; Residues: 23-45 <STE>
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Best Local S
Matches 81
                                                                                                                                                                            21
                                                                                                                                                                                                                                                                                                                289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73 RWAGMGRRILLIRSVQLHDSGNYSCYRAGRPAGTVHLLV------DV-----PPEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16 LASPLVAIWELKKDVYVVELDWYPDAPGEMVVLTCDTPE-EDGIT--WTL-----DQSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 LAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHWVLRKPAAGSHPS
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                                                                                                                                                                                                                                                                                                                                                                                   CVIHDAWSGL----RHVVQLRAQEEFGQGEWSEWS 307
                                                                                                                                                                                                                                                                                                   - VFTDKTSATVICRKNASISVRAQDRYYSSSWSEWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NLQLKPL-KNSRQVEVSWEYPDTWSTPHSYFSLTFCVQVQGKSKREK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NITVTAVARNPRWLSVTWQDPHSWNS--SFYRLRF--ELRYRAERSKTFTTWMVKDLQHH 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Y----EYSVECQEDS---ACPANEESLPIEVMVDAVHKLKYENYTSSFFIRDIIKPDPPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FQEPCQYSQESQKFSCQLAVPEGDSSFYIVSMCVASSVGSKFSKTQTFQGCGILQPDPPA
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#sequence_revision
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                                                                                            chicken
    30-Sep-1993
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#text_change
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    09-Jul-2004
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A;Title: Cloming, expression, and mutational analysis of the A;Reference number: I50455; MUID:94283267; PMID:7516866
A;Accession: I50455
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        prolactin receptor - pigeon
c;Species: Columba livia (domestic pigeon)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: I50455
R;Chen, X; Horseman, N.D.
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A;Cross-references: UNIPROT:Q04594; DDBJ:D13154; NID:g222848; PIDN:BAA02439
A;Experimental source: kidney
C;Keywords: glycoprotein; transmembrane protein
F;1-23/Domain: signal sequence #status predicted <SIG>F;24-831/Product: prolactin receptor #status predicted <MAT>F;26-219/Domain: cytokine receptor homology <CRS1>F;36-219/Domain: cytokine receptor homology <CRS1>F;39-425/Domain: cytokine receptor homology <CRS2>F;439-462/Domain: transmembrane #status predicted <TMM>F;439-462/Domain: transmembrane #status predicted <TMM>F;439-462/Domain: transmembrane #status predicted <TMM>F;439-462/Domain: cytokine receptor homology <CRS1>F;439-462/Domain: transmembrane #status predicted <TMM>F;439-462/Domain: transmembrane #status predicted <TMM>F;439-462/Domain: cytokine receptor homology <CRS1>F;439-452/Domain: transmembrane #status predicted <TMM>F;439-452/Domain: cytokine receptor homology <CRS1>F;439-452/Domain: cytokine receptor homology <CRS1
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A;Residues: 1-830 <CHE>
A;Cross-references: UNIPROT:Q90374; EMBL:U07694; NID:g466381; PIDN:AAA20646.1; PID:g46638F;36-220/Domain: cytokine receptor homology <CRS1>
F;36-220/Domain: cytokine receptor homology <CRS2>
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R;Tanaka, M.; Maeda, K.; Okubo, T.; Nakashima, K.
Biochem. Biophys. Res. Commun. 188, 490-496, 1992
A;Title: Double antenna structure of chicken prolactin receptor deduced from A;Reference number: JQ1655; MUID:93075121; PMID:1445292
A;Accession: JQ1655
A;Accession: JQ1655
A;Accession: JQ1655
A;Accession: JQ1655
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308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        102 PAGTVHLLVDVPPEEPQLSCFRKSPLSNVVCEWGPRSTPSLTTKAVLLVRKFQNSPAEDF 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
KATNEIGSNVSDPLYVDVTYIVQTDPPVNVTLELKKTVNRKP-YLVLTWSPPPLADVRSG
                                                                 CVASSVGSKFSKTQTFQGCGILQPDPPANITV---TAVARNPRWLSVTWQDP--HSWNSS
                                                                                                                                                                                                               VLLVRKFQNSPAEDFQEPCQYSQESQK--FSCQLAVPEGDSSFYI------VSM
                                                                                                                                                                                                                                                                                           DIGEWSEWSSER-----HIHIPNGESPPEKPTIIKCRSPEKETFTCWWKPGSDGGHPTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTWMVKDLQHHCVIHDAWSGLRHVVQLRAQEEFGQGEWSEWSPE
                                                                                                                                                                                                                                                                                                                                                            DSGNYSCYRAGRPAGTVHLLV---DVPPEEPQLSCFRKSPLSNVVCEWGPRSTPSLTTKA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VDVTSIVQPGSPVNLTLETKRSANIMYLWAKWSPPLLADASSNHLYHYELRIKPEEKEEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FQGCGILQPDPPANITV-TAVARNPRWLSVTWQDPHSWNSSFYRL-RFELRYRAERSKTF 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----YSKDSEEEIYECPDYRTSGPNSCYFNKNHTSPWTTFNITVTATNEIGSNSSDPQY
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27.2%; Pred. No. 0.00016;
vative 31; Mismatches 96
                                                                                                                                                                                                                                                                                                                                                                                                                                     6.2%; Score 178.5; DB 22.0%; Pred. No. 0.0002; tive 55; Mismatches 15
                                                                                                                                      SKEGEERVYECPDYKTAGPNSCYFDKKHTSFWTIYNITV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                         158;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         107;
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171

275 275 220 216

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glycoprotein 130 - mouse
C.Species: Mus musculus (house mouse)
C.Species: Mus musculus (house mouse)
C.Date: 02-Aug-1906 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C.Accession: I49699; I48370
R.Saito, M.; Yoshida, K.; Hibi, M.; Taga, T.; Kishimoto, T.
J. Immunol. 148, 4066-4071, 1992
A.;Title: Molecular cloning of a murine IL-6 receptor-associated signal transducer,
A.Reference number: I48370; MUID:92291532; PMID:1602143
A.Recession: I49699
A.;Status: translated from GB/EMBL/DDBJ
A.;Molecule type: mRNA
A.;Molecule type: mRNA
A.;Residues: 1-917 <RES>
A.;Cross-references: UNIPROT:Q00560; GB:M83336; NID:g193591; PIDN:AAA37723.1; PID:g1
A.;Accession: I48370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Scott, P.; Kessler, M.A.; Schuler, L.A.
Mol. Cell. Endocrinol. 89, 47-58, 1992
A;Title: Molecular cloning of the bovine prolactin receptor A;Reference number: I45971; MUID:93246019; PMID:1338725
A;Accession: I45971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        prolactin receptor - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C;Accession: I45971
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 6.0%; Score 171; DB 2; Best Local Similarity 25.0%; Pred. No. 0.00041; Matches 51; Conservative 40; Mismatches 99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PLTSSERIDKQI-RYILDGISALRKETCNKSNMCESSKEA-----LAENN 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RKPYLWIKWSPPTMTDVKSGWFIIQYEIRLKPEKATDWETHFTLKQTQ--LKIFNLYPGQ
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Cross-references: EMBL:X62646; NID:g840816; PIDN:CAA44515.1; PID:g840817
C;Genetics:
C;Genetics:
A;Gene: gp130
C;Keywords: glycoprotein
C;Keywords: glycoprotein
C;Keywords: glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cell 63, 1149-1157, 1990
A;Title: Molecular cloning and expression of an IL-6 signal transducer, A;Reference number: A36337; MUID:91084844; PMID:2261637
A;Accession: A36337
A;Accession: A36337
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-918 <hi>HIB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 25
A36337
R;Hibi, M.; Murakami, M.; Saito, M.; Hirano, T.; Taga, T.; Kishimoto, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: GDB:IL6ST; GP130
A;Cross-references: GDB:126725; OMIM:600694
A;Map position: 5q11-5q11
C;Keywords: glycoprotein; membrane protein
F;134-316/Domain: cytokine receptor homology
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C;Genetics:
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                                                    281
                                                                                                 274
                                                                                                                                                                                                                                      172 ----CKAKRDTPT-SCTVDY----STVYFVNIEVWVEAENALGKVTSDHINFDPVYKVKP
                                                                                                                                                                                                                                                                                                                               118 ITIISGLPPEKPKNLSCIVNEG-KKWRCEWDGGRETHLETNFTLKSEWATHKFAD----
                                                                                                                                                                                                                                                                                                                                                         106 VHLLVDVPPEEP-QLSCFRKSPLSNVVCEWGP-RST---PSLTTKAVLLVRKFQNSPAED 160
                                                                                                                                                                                         217 DPPANITYTAVARNPRWLSYTWODPHSWNSSFYRLREELRYRAERSKTFTTWMVKD---L
                                                                                                                                                                                                                                                                                                                                                                                                                       82;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VTMLSGFPPDKPTNLTCIVNEG-KNMLCQWDPGRETYLETNYTLKSEWATEKFPD-----
                                                                                            QHHCVIHDAWSGLRHVVQLRAQEEFGQGEWSEWSPEAMGTPWTE--SRSP-----PAE 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MSPRTSFTVQDLKPFTEYVFRIRSIKDSGKGYWSDWSEEASGTTYEDRPSRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DPPANITVTAVARNPRWLSVTWODPHSWNSSFYRLRFELRYRAERSKTFTTWMVKDLQH-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FQEPCOYSQESQKFSCQLA-VPEGDSSFYI---VSMCVASSVGSKFSKTQTFQGCGILQP
                                                                                                                                                                                                                                                                                 FQEPCQYSQESQKFSCQLAVPEGDSSFYIVSMCV----ASSVGSKFSKTQTFQGCGILQP
         NE---
                                                    RSSFTVQDLKPFTEYVFRIRCMKEDGKGYWSDWSEEASGITYEDRPSKAPSFWYKIDPSH 340
                                                                                                                                            NPPHNLSVINSEELSSILKLTWTNPSI--KSVIILKYNIQYRTKDASTWSQIPPEDTAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----HCVIHDAWSGLRHVVQLRAQEEFGQGEWSEWSPEAMGTPWTESRSPP 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TPPYNLSVINSEELSSILKLSWVS--SGLGGLLDLKSDIQY---RTKDASTWIQVPLEDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.9%; Score 167.5; ilarity 25.0%; Pred. No. 0.0 Conservative 48; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                       5.9%; Score 167.5; DB 2; ilarity 22.1%; Pred. No. 0.0013; Conservative 61; Mismatches 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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           -LTINKDDD--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      interleukin-6 signal transducing molecule gp130 - rat C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A44257
R;Wang, Y:, Nesbitt, J.E.; Fuentes, N.L.; Fuller, G.M.
Genomics 14, 666-672, 1992
A;Title: Molecular cloning and characterization of the rat liver IL-6 signa A;Reference number: A44257; MUID:93052397; PMID:1427893
A;Accession: A44257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-918 <WAN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Keywords: transmembrane protein
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   528
                                                                     481
                                                                                         446 IITGLLEFEVYLEYLQNRFESSEEQARAVQMSTKVLIQFLQKKAKNLDAITTPDPTTNAS
                                                                                                                                         451
                                                                                                                                                                            386
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                                                                                                                                                                                                                                                                                                                                                                                                                                           217 DPPANITVTAVARNERWLSVTWQDPHSWNSSFYRLRFELRYRAERSKTFTTWMVKDLQH-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 106 VHLLVDVPPEEP-QLSCFRKSPLSNVVCEWGP-RST---PSLTTKAVLLVRKFQNSPAED
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                                  LLTKLQAQNQW 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
KVGKNEAVLEW 538
                                                                LRGSLLESKCYLITVTPVFPGGPGSPESM-
                                                                                                                                      ---KYIL-----EWC----
                                                                                                                                                               KQIRYILDGISALRKETCNKSNMCESSKEALAENNLNLPKMAEKDGCFQSGFNEETCLVK 445
                                                                                                                                                                                                ASLAARNVVGKSPATVLTIPGSHFKASHPVVDLKAFPKDNLLWVEWTPPSKPVN-----
                                                                                                                                                                                                                                                                    ANHPQEYRSARLIWKTLPLSEANGKILDYEVVLTQSKSVSQTYTVNGTELIVNLTNNRYV
                                                                                                                                                                                                                                                                                                                                        VSPRTSFTVQDLKPFTEYVFRIRSIKENGKGYWSDWSEEASGTTYEDRPSKAPSFWYKVN
                                                                                                                                                                                                                                                                                                                                                                       -----HCVIHDAWSGLRHVVQLRAQEEFGQGEWSEWSPEAMGTPWTE--SRSP-----
                                                                                                                                                                                                                                                                                                                                                                                                            SPPHNLSVTNSEELSSILKLAW--VNSGLDSILRLKSDIQY---RTKDASTWIQVPLEDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FQEPCQYSQESQKF$CQLAVPEGDSSFYIVSMCV----ASSVGSKF$KTQTFQGCGILQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ITILSGYPPDIPTNLSCIVNEG-KNMLCQLDPGRETYLETNYTLKSEWATEKPPD-----
                                                                                                                                                                                                                                       ----DNILFRDSANATSLP-VEFMPVPPGEDSKDVA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----CRTKHGTS--SCMM----GYTPIYFVNIEVWVEAENALGNVSSEPINFDPVDKVKP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---NILFRDSANATSLPV-EFMPVPPGEDSKDVAAPHRQPL----TSSERIDKQIRYIL 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TQGYRTVQLVWKTLPPFEÄNGKILDYEVTLTRWKSHLQNYTVNATKLTVNLTNDRYLATL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cytokine receptor homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.8%; Score 166; DB 2; 20.2%; Pred. No. 0.0017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71; Mismatches 171; Indels 150;
                                                                                                                                                                                                                                                                                                         -----NEVSTPMOALTTNKDD------
                                                                                                                            -VLSENSPCIPDWQQEDGTVNR-----
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                                                            -KAYLKQAAPSKGPTVRTK 527
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A;Molecule type: protein
A;Molecule type: protein
A;Notes: the samino end of the mature protein was blocked
C;Keywords: blocked amino end; glycoprotein; transmembrane protein
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-616/Product: prolactin receptor 2 #status predicted <MAT>
F;36-221/Domain: transmembrane #status predicted <TMM>
F;25-58/Domain: transmembrane #status predicted <TMM>
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A;Title: Purification and partial sequence of the rabbit mamma A;Reference number: A60380; MUID:91146782; PMID:2289615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prolactin receptor 2 precursor - rabbit
N;Alternate names: prolactin receptor, mammary gland
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Accession: A30304; A60380
R;Edery, M; JOlicoeur, C; Lievi-Meyrueis, C; Dusanter-Fourt, I; Petridou, B; Boutin, Proc. Natl. Acad. Sci. U.S.A. 86, 2112-2116, 1989
A;Title: Identification and sequence analysis of a second form of prolactin receptor by A;Reference number: A30304; MUID:89184578; PMID:2928321
A;Reference number: A30304; MUID:89184578; PMID:2928321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: A60380
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A;Residues: 1-616 <ED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
EVDDSEDQQLMPAHSKEHSGPGMKP 340
                                             PVPPGED-----
                                                                                           GYSMVTCIFPP--
                                                                                                                          GTPWTESRSPPAENEVSTP-----MQALTTNKDDDNIL----FRDSANATSLPVEFM
                                                                                                                                                                     YLVQVRCKPD--HGFWSVWSPESSIQIPNDFTMKDITVWIFVAVLSTIICLIMVWAVALK 259
                                                                                                                                                                                                                          HVVQLRAQEEFGQGEWSEWSPEA-----
                                                                                                                                                                                                                                                              RKPYLWVKWLPPTLVDVRSGWLTLQYEIRLKPEKAAEWETHFAGQ-QTQFKILSLYPGQK 201
                                                                                                                                                                                                                                                                                                         R--WLSVTWODPH--SWNSSFYRLRFELRYRAERSKTFTTWMVKDLOHHCVIHDAWSGLR 287
                                                                                                                                                                                                                                                                                                                                                      PNSCYFSKKHTSIWTIYIITVNATNQMGSSVSDPRYVDVTYIVEPDPPVNLTLEVKHPED
                                                                                                                                                                                                                                                                                                                                                                                                  KFSCQLAVPEGDS-SFYIVSMCVASSVGSKFSKTQTFQGCGILQPDPPANITVTAVARNP
                                                                                                                                                                                                                                                                                                                                                                                                                                             PPGKPFIFKCRSPEKETFTCWWRPGADGGLPTNYTLTYHK----EGETITHECPDYKTGG 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PPEEPQLSCFRKSPLSNVVCEWGPRSTPSLTTKAVLLVRKFQNSPAEDFQEPCQYSQESQ 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.6%; Score 161.5; DB 21.8%; Pred. No. 0.002; tive 42; Mismatches 1
                          ·SKDVAAPHRQP
||::| ;|
                                                                               --VPGPKIKGFDTHLLEKGKSEELLSAFGCQDFPPTADCEDLLVEFL
                                        377
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C;Accession: A29884
C;Accession: A29884
R;Boutin, J.M.; Jolicoeur, C.; Okamura, H.; Gagnon, J.; Edery, Cell 53, 69-77, 1988
Cell 53, 69-77, 1988
A;Title: Cloning and expression of the rat prolactin receptor, A.Bafarence number: A29884; MUID:88165059; PMID:2832068

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M.; Shirota, M.; Banville,

A; Cross-references: UNIPROT: P05710;

GB:M19304; NID:g206364;

PIDN:AAA41937.1;

PID: g206365

A; Molecule type: mRNA A; Residues: 1-310 < BOU> prolactin receptor precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep_1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004

RESULT 28 A29884

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A;Cross-references: UNIPROT:P05710; GB:M74152; NID:g206389; PIDN:AAA41946.1; PID:g206390 R;O'Neal, K.D.; Yu-Lee, L.Y.
J. Biol. Chem. 269, 26076-26082, 1994
A;Title: Differential signal transduction of the short, Nb2, and long prolactin receptor A;Reference number: I55417; MUID:95014432; PMID:7929319
A;Accession: I55417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Rattus norvegicus (Norway rat)
C;Date: 12-Jun-1992 #sequence revision 12-Jun-1992 #text_change 09-Jul-2004
C;Accession: A41070; IS4417
R;Ali, S; Pellegrini, I:; Kelly, P.A.
J. Biol. Chem. 266, 20110-20117, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: A prolactin-dependent immune cell line (Nb2) expresses A;Reference number: A41070; MUID:92041834; PMID:1718958 A;Accession: A41070
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C;Species: Rattus norverier: '"
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A,Molecule type: mRNA
A,Residues: 1-412 <RES>
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A; Residues: 1-412 < ALI>
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Best Local :
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182
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                                 HHC--VIHDAWSGLRHVVQLRAQEEFGQGEWSEWSPEA 310
                                                                                                                                                                                      K--FSCQLAVPEGDSS------FYIVSMCVASSVGSKFSKTQTFQGCGILQPDP
                                                                                                                                                                                                                                                                PPEEPOLSCFRKSPLSNVVCEWGPRSTPSLTTKAVLLVRKFQNSPAEDFQEPCQYSQESQ
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                                                                                                             PANIT--VTAVARNPRWLSVTWQDP--HSWNSSFYRLRFELRYRAERSKTFTTWMVKDLQ 274
                                                                                                                                                  KTTYECPDYKTSGPNSCFFSKQYTSIWKIYIITVNATNQMGSSSSDPLYVDVTYIVEPEP
                                                                                                                                                                                                                              PPGKPEIHKCRSPDKETFTCWWNPGTDGGLPTNYSL-----TYSKEGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PANIT -- VTAVARNPRWLSVTWODP -- HSWNSSFYRLRFELRYRAERSKTFTTWMVKDLQ 274
                                                                         PRNLTLEVKQLKDKKTYLWVKWSPPTITDVKTGWFTMEYEIRLKPEEAE---EWEIHFTG
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22.5%;
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Pred. No. 0.0012;
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A;Molecule type: mRNA
A;Residues: 1-610 <ZHA>
A;Residues: 1-610 <ZHA>
A;Cross-references: UNIPROT:P05710; GB:M34083; NID:g205122; PIDN:AAA79273.1; PID:g205123
A;Note: the authors translated the codon GAG for residue 533 as Gly
F;31-216/Domain: cytokine receptor homology <CRS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Shirota, M.; Banville, D.; Ali, S.; Jolicoeur, C.; Boutin, J Mol. Endocrinol. 4, 1136-1143, 1990
Mol. Endocrinol of two forms of prolactin receptor in rat A;Reference number: A36116; MUID:91155946; PMID:2293022
A;Accession: A36116
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prolactin receptor 2 precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Mar.1991 #sequence_revision 28
C;Accession: A36116
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A36116
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A34631
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A;Residues: 1-610 <SHI>
A;Cross-references: UNIPROT:P05710; GB:M57668; NID:g206366; PIDN:AAA41938.1; PID:g206367;
F;31-216/Domain: cytokine receptor homology <CRS>
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                                          219 PANIT--VTAVARNPRWLSVTWODP--HSWNSSFYRLRFELRYRAERSKTFTTWMVKDLQ 274
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PRNLTLEVKQLKDKKTYLWVKWSPPTITDVKTGWFTMEVEIRLKPEEAE---EWEIHFTG 181
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                                                                                       KTTYECPDYKTSGPNSCFFSKQYTSIWKIYIITVNATNQMGSSSSDPLYVDVTYIVEPEP
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22.5%;
                                                                                                                                                                                                                                                                      5.6%; Score 159; DB 2; Length 610 22.5%; Pred. No. 0.003; Indels
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Pred. No. 0.003;
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293 208

401

250 349

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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-630 <SAN>
A;Cross-references: UNIPROT: 091513; GB:L34783; NID: g903846; PID: g903847
F;37-222/Domain: cytokine receptor homology <CRS>
                                                                                                                                                                                                                           C;Accession: 151086
R;Sandra, O.; Sohm, F; de Luze, A.; Prunet, P.; Edery, M.; Kelly, P.A.
Proc. Natl. Acad. Sci. U.S.A. 92, 6037-6041, 1995
A;Title: Expression cloning of a cDNA encoding a fish prolactin receptor.
A;Reference number: I51086; MUID:95320210; PMID:7597076
A;Accession: I51086
                                                                                                                                                                                                                                                                                                                                             prolactin receptor - Nile tilapia
C;Species: Tilapia nilotica, Oreochromis niloticus
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996
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C;Species: Mus mus
C;Species: 02-Aug-19;
C;Accession: I727/
R;Schoenhaut, D.S
J. Immunol. 148;
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A;Molecule type: mRNA
A;Residues: 1-335 <RES>
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A;Reference number: I56135; MUID:92268481; PMID:1350290
A;Accession: I72789
                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPROT:P43432; GB:M86671; NID:g293663; PIDN:AAA39296.1; PID:g293664
                                                                                                        Query Match
Best Local :
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Best Local !
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/Species: Mus musculus (house mouse)
/Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
/Accession: I72789
                                                                                                    Local
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           81 LLLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPEEPQLSCFRKSPLSNVVCEWGPRSTP 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GLRHVVQLRAQEEFGQGEWSEWS 307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----GPRSTP-----SLTTKAVLLVRKFQNSPAEDFQEPCQYSQESQKFSCQ--L 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HKGGETLSHSHLLLHKKENGIWSTEILKNFKNKTFLKCEAPNYSGRFTCSWLVQRNMDLK 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YRAGRPAGTVHLLVDVP------PEEPQLSCFRKSPLSNVVCEW-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PGETVNLTCDTPEEDD---ITWTSDQRHGVIGS-----GKTLTITVKEFLDAGQYTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D.S.; Chua, A.O.; Wolitzky, A.G.; Quinn, 48, 3433-3440, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HQTQFKVFDLYPGQKYLVQTRCKPD--HGYWSRWSQES
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                                                                                Conservative
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                                                                                                                   5.5%;
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                                                                              52;
                                                                         Score 158; DB
Pred. No. 0.003
52; Mismatches
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                                                                                            DB 2;
                                                                           152;
                                                                                                                                                                                                                                                                                                                                           (Nile tilapia) #text_change 0
                                                                                                           Length 630;
                                                                     Indels 108;
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prolactin receptor precursor - mouse C;Species: Mus musculus (house mouse) C;Date: 02-Aug-1996 #sequence_revision C;Accession: I77524 R;Davis, J.A.; Linzer, D.I.H. Mol. Endocrinol. 3, 674-680, 1989
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A;Title: Expression of multiple forms of the prolact A;Reference number: 157699; MUID:89261824; PMID:272: A;Accession: 177525
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: UNIPROT:Q08501; GB:M22959; NID:g200481; PIDN:AAA39977.1; PID:g200482
F;31-216/Domain: cytokine receptor homology <CRS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    prolactin receptor precursor - mouse C;Species: Mus musculus (house mouse) C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 C;Accession: I77525 R;Davis, J.A.; Linzer, D.I.H. Mol. Endocrinol. 3, 674-680, 1989
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177525
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A; Residues: 1-292 < RES>
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                                                                                                                                                                                                                 HHC--VIHDAWSGLRHVVQLRAQEEFGQGEWSEWSPE 309
                                                                                                                                                                                                                                                  PRNITLEVKQLKDKKTYLWVKWLPPTITDVKTGWFTMEYEIRLKSEEA---DEWEIHFTG 181
                                                                                                                                                                                                                                                                                                                                                        K--FSCQLAVPEGDSS------FYIVSMCVASSVGSKFSKTQTFQGCGILQPDP 218
                                                                                                                                                                                                                                                                                   PANIT--VTAVARNPRWLSVTWODP--HSWNSSFYRLRFELRYRAERSKTFTTWMVKDLQ
                                                                                                                                                                                                                                                                                                                        KNTYECPDYKTSGPNSCFFSKQYTSIWKIYIITVNATNEMGSSTSDPLYVDVTYIVEPEP
                                                                                                                                                                                                                                                                                                                                                                                             PPGKPEIHKCRSPDKETFTCWWNPGSDGGLPTNYSL-----TÝSKEGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CKPD--HGFWSBWS-----STSYVKVP-EYLHREKSVWILVLVFSAFILL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.4%; Score 155; DB 2; 22.6%; Pred. No. 0.0021; tive 35; Mismatches 91
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                                                02-Aug-1996 #text_change
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4; PMID:2725531
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                                                     09-Jul-2004
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mouse

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A;Molecule type: mRNA
A;Residues: 1-557, Fr,559-608 <EDE>
A;Residues: 1-557, Fr,559-608 <EDE>
A;Residues: 1-557, Fr,559-608 <EDE>
A;Cross-references: EMBL:X73372; NID:g312696; PIDN:CAA51789.1; PID:g312697
A;Cross-references: EMBL:X73372; NID:g312696; PIDN:CAA51789.1; PID:g312697
C;Comment: Prolactin receptor have long form and short form which are result;
C;Comment: This long form receptor is capable of transducing a signal to m:
C;Comment: This long form receptor protein
C;Keywords: receptor; transmembrane protein
F;31-216/Domain: cytokine receptor homology <CRS>
F;230-253/Domain: transmembrane #status predicted <TMM>
                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:L13593; NID:g347398; PIDN:AAC37641.1; PID:g347842 R;Edery, M.; Pezet, A.; Nandi, S.; Kelly, P.A. submitted to the EMBL Data Library, June 1993 A;Description: Isolation and nucleotide sequence of a mouse cDNA prolact.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gene 134, 263-265, 1993
A;Title: Cloning and sequencing of the cDNA encoding the A;Reference number: JT0671; MUID:94085788; PMID:8262385
A;Accession: JT0671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Mus musculus (house mouse)
C;Date: 02-Aug-1996 #sequence revision 02-Aug-1996 #text_change 09-Jul-2004
C;Accession: I53299; JT0671; S34356
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A; Residues: 1-608 < MOO>
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R;Moore, R.C.; Oka, T.
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A; Residues: 1-608 < RES>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Endocrinology 133, 224-232, 1993
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C;Species: Mus muscu
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A; Residues: 1-303 < RES>
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Best Local Similarity
Matches 49; Conserv
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HQTQFKVFDLYPGQKYLVQTRCKPD--HGYWSRWGQE 216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PANIT -- VTAVARNPRWLSVTWQDP -- HSWNSSFYRLRFELRYRAERSKTFTTWMVKDLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KNTYECPDYKTSGPNSCFFSKQYTSIWKIYIITVNATNEMGSSTSDPLYVDVTYIVEPEP
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                                                                                        5.4%;
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                                                                 Score 155; DB
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35; Mismatches
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5; Mismatches
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                                                                                      DB 2;
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A;Cross references: UNIPROT:Q06418; GB:U05682; NID:g463469; PIDN:A R;Ohashi, K.; Mizuno, K.; Kuma, K.; Miyata, T.; Nakamura, T. Oncogene 9, 699-705, 1994
A;Title: Cloning of the cDNA for a novel receptor tyrosine kinase, A;Fatle: Cloning of the cDNA for a novel receptor tyrosine kinase, A;Reference number: JP0077; MUID:94150991; PMID:8108112
A;Accession: JP0077
A;Molecule type: mRNA
A;Fesidues: 1-890 < COHA>
A;Cross-references: DDBJ:D17517; NID:g624880; PIDN:BAA04467.1; PID A;Experimental source: hepatoma HepG2 cell
R;Folvi, A; Armstrong, E; Lai, C.; Lemke, G.; Huebner, K.; Sprit: Gene 134, 289-293, 1993
A;Fitle: The human TYRO3 gene and pseudogene are located in chromota; A;Reference number: JC2145; MUID:94085793; PMID:8262388
A;Accession: JC2145
A;Molecule type: mRNA
A;P6014016-11-700
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A;Reference number: S3:
A;Accession: S32765
A;Status: preliminary
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A,Residues: 519-790 <POL>
A,Cross-references: EMBL:X72886; NID:g296020; PIDN:CAA51396.1;
R;Polvi, A.; Armstrong, E.; Lai, C.; Lemke, G.; Huebner, K.; Al
submitted to the EMBL Data Library, March 1993
A,Description: Human Tyro3 gene and pseudogene in chromosome 15
A;Reference number: S32219
F;42-890/Product: protein-tyrosine kinase tyro3 #status predic
F;60-119/Domain: immunoglobulin homology <IMM1>
F;156-205/Domain: immunoglobulin homology <IMM2>
F;156-205/Domain: fibronectin type III repeat homology <FN3A>
F;322-405/Domain: fibronectin type III repeat homology <FN3B>
F;429-491/Domain: transmembrane #status predicted <TMM>
F;429-491/Domain: brotein kinase homology <KIN>
F;516-793/Domain: protein kinase homology <KIN>
F;524-532/Region: protein kinase ATP-binding motif
F;63,191,230,240,293,366,380/Binding site: carbohydrate (Asn)
                                                                                                                                                                                                                                                                                                                                       A;Gene: GDB:TYRO3
A;Cross-references: GDB:134764; OMIM:600341
A;Cross-references: GDB:134764; OMIM:600341
A;Map position: 15q15.1-11q21.1
C;Superfamily: protein-tyrosine kinase axl; fibronectin type III repeat homology; C;Keywords: ATP; brain; glycoprotein; growth factor receptor; phosphotransferase; F;1-41/Domain: (or 7-41) signal sequence #status predicted c5IG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:X72886; NID:g296020; PIDN:CAA51396.1; PID:g312336
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A; Residues: 519-790 <
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A; Accession: A53743
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein-tyrosine kinase (EC 2.7.1.112) tyro3 precursor - human
N;Alternate names: protein-tyrosine kinase sky; receptor-type
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Down syndrome cell adhesion protein 1 - human (fragment)
N;Alternate names: Down syndrome cell adhesion molecule
N;Alternate names: Down syndrome cell adhesion molecule
C;Species: Homo sapiens (man)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 11-Jun-1999
C;Accession: T08851
R;Yamakawa, K; Hubo, Y.K.; Haendel, M.A.; Hubert, R.; Chen, X.N.; Lyons, G.E.; Korer
submitted to the EMBL Data Library, September 1997
A;Description: DSCAM: A novel member of the immunoglobulin superfamily maps in a down; A;Reference number: 216495
A;Accession: T08851
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Coss-references: EMBL;AF023449; NID:g3169765; PID:g3169766
A;Cross-references: EMBL;AF023449; NID:g3169765; PID:g3169766
A;Cross-references: EMBL;AF023449; NID:g3169765; PID:g3169766
A;Cross-references: EMBL;AF023449; NID:g3169765; PID:g3169766
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Best Local
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VVQNLDQLYIPVSEQH---WIGF---LSLKSVERSDAGRYWCQVEDGGETEISQEVWLTV 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LGLLLAALASLLLPESAAAGLKLMGAPVKLTVSQGQPVKLNC-SVEGMEEPDIQWVKDGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----LRKPAAGSHPSRWAGMGRRLLLRSVQLHDSGNYSCY------RAGRPA----
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                                                                                                                                                                                                                                                              5.0%;
Similarity 23.8%;
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                                                                                                                                                                         RCPAQEVA-RGVLTSLPGDSVTLTCPGVEPEDNATVHWVLRKPAAGSHPSRWAGMGRR--
                                                                                                       FSNGSFIIRTVKAEDSGYYSCIANNNWGSDEIILNLQVQVPPDQPRLT-VSKTTSSSITL 138:
                                                                                                                                      -----LLLRSVQLHDSGNYSCY---RAGRPAGTVHLLVDVPPEEPQLSCFRKSPLSNVVC 132
 VPEGDSSFYIVSMCVASSVGS--KFSKTQTFQGCGILQPDPPANITVTAVARNPRWLSVT 237
                                    SWILPGDNGGSSIRGYILQYSEDNSEQWGSFPISPSER----SYRLENLKCGTWYKFTLT 1438
                                                                       EWGPRSTPSLTTKAVLLVRKFQN------
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                                                                                                                                                                                                                                                     49;
                                                                                                                                                                                                                                                 Score 144; DB 2; I
Pred. No. 0.15;
19; Mismatches 153;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLLRDLVPATNYSLRVRCANALGPSPYADWVP
                                                                           -SPAEDFQEPCQYSQESQK----FSCQLA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 119;
                                                                                                                                                                                                                                                                                    Length 1896;
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RESULT 39
B59405
B59405
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #to
C; Accession: B59405; B49400
R; Hu, Z.Z.; Meng, J.; Dufau, M.L.
J. Biol. Chem. 276, 41086-41094, 2001
A; Title: Isolation and characterization of two novel:
A, Reference number: A59405; MUID:21538812; PMID:11518
A, Accession: B59405
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A;Reference number: B49400
A;Status: preliminary
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-280 <4H72>
A;Residues: 1-280 <4H72>
A;Residues: 1-280 <4H72>
A;Cross-references: GB:AF214012; PIDN:AF214012.1
A;Cross-references: GB:AF214012; PIDN:AF214012.1
C;Comment: This is one of the short forms (S1a and S1b) of the human proactin receptor 90 ta-casein gene promoter activation, with S1b more effective than S1a. However, their ligital-casein gene promoter activation, with S1b more effective than S1a. However, their ligital-casein gene promoter activation, with S1b more effective than S1a.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-288 < HU1>
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A;Map position: 5p13.3-5p13.1

C;Keywords: glycoprotein; transmembrane predicted <SIG>
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-288/Product: prolactin receptor, short form S1b #status predicted <MAT>
F;25-288/Product: prolactin receptor homology <CRS>
F;36-221/Domain: cytokine receptor homology <CRS>
F;59,104,233/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Genetics:
A;Gene: GDB:PRLR
A;Cross-references: GDB:120315; OMIM:176761
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submitted to GenBank, December, 1999
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prolactin receptor short form Sla precursor, breast cancer cells
C;Species: Homo sapiens (man)
C;Date: 01-Peb-2002 #sequence_revision 01-Peb-2002 #text_change 0
C;Accession: A59405; A49400
                                                                                            RESULT
A59405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WODEHSWNSSEYRLRFELRYRAERSKTFTTWMVKDLQHHCVIHDAWSGLRHVVQLRAQEE 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VPPEEPQLSCFRKSPLSNVVCEWGPRSTPSLTTKAVLLVRKFQNSPAEDFQEPCQYSOES 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LPPGKPEIFKCRSPNKETFTCWWRPGTDGGLPTNYSLTYHR-
                                                                                                                                                                                                                                                                                                                                                                                LMHECPDYITGGPNSCHFGKQYTSMWRTYIMMVNATNQMGSSFSDELYVDVTYIVQPDPP
                                                                                                                                                                                                                                                                                                                                   ANITVTAVARNER--WLSVTWODEH--SWNSSEYRLREELRYRAERSKTETTWMV-----
                                                                                                                                                                                                                                                                                                                                                                                                                             OKFSCQLAVPEGDSS-----
                                                                                                                                                                                                                                       ---- KDLOHHCVIHDAWSGLRHVVOLRAQEEFGQGEWSEWSP
                                                                                                                                                                                                                                                                                      LELAVEVKQPEDRKPYLWIKWSPPTLIDLKTGWFTLLYEIRLKPEKA---AEWEIHFAGQ
                                                                                                                                                                                             QTEFKILSLH-----
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                                                                                                                                                                                                  -PGOKYLVOVRCKPD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 138; DB 2; Pred. No. 0.031; 32; Mismatches
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A;Map position: 5p13.5-5p13.1
C;Keywords: glycoprotein; transmembrane protein
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-376/Product: prolactin receptor, short form S1a #status predicted <MAT>
F;36-221/Domain: cytokine receptor homology <CRS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:AF214012; PIDN:AF214012.1
C;Comment: This is one of the short forms (S1a and S1b) of the human prolactin receptor eta-casein gene promoter activation, with S1a less effective than S1b. However, their lited COS-1 and HEK293 cells is due to rapid intracellular turnover of the receptor. #expe
Search completed: December Job time : 51.8543 secs
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A;Molecule type: DNA
A;Residues: 1-376 <HU2>
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A;Reference number: A49400
A;Accession: A49400
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J. Biol. Chem. 276, 41086-41094, 2001
A;Title: Isolation and characterization of two novel forms of the human prolactin recept A;Reference number: A59405; MUID:21538812; PMID:11518703
A;Accession: A59405
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Matches 49
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Varghese J.N., Moritz R.L., Lou M.-Z., Van Donkelaar A.,
Ivancic N., Branson K.M., Hall N.E., Simpson R.J.;
"Structure of the extracellular domains of the human into
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- TISSUE SPECIFICITY: Isoform 2 Is expressed in peripheral blood
- TISSUE SPECIFICITY: Isoform 2 Is expressed in peripheral blood
- TISSUE SPECIFICITY: Isoform 2 Is expressed in peripheral blood
- TISSUE SPECIFICITY: Isoform 2 Is expressed in peripheral blood
- TISSUE SPECIFICITY: Isoform 2 Is expressed in peripheral in
- DOMAIN: The two fibronectin type III-like domains, contained in
- DOMAIN: The WSWS motif appears to be necessary for proper protein
- DOMAIN: The WSWS motif appears to be necessary for proper and cell-
- BOMAIN: The WSWS motif appears to be necessary for proper and cell-
- STATE TO SET 
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c. Natl. Acad. Sci. U.S.A. 99:15959-15964(2002).
epincarion: Fundamental academic activation may activation necessitate an association with ILGST. Activation may activation necessitate an association with ILGST. Activation may lead to the regulation of the immune response, acute-phase lead to the regulation of the immune response.
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FUNCTION: Low concentration of a soluble form (
FUNCTION: Low concentration of IL6 activity.

receptor acts as an agonist of IL6 activity.

SUBUNIT: Hexamer of two molecules each of IL6,

SUBCELLULAR LOCATION: Type I membrane protein

Secreted (isoform 2).

ALTERNATIVE PRODUCTS:
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IsoId=P08887-1; Sequence=Displayed;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: Contains 1 fibronectin type III domain. SIMILARITY: Contains 1 immunoglobulin-like C2-type domain. DATABASE: NAME=PROW; NOTE=CD guide CD126 entry: WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd126.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 K., Natsuka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S
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                                                                                                                   linked signal transdu.
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InterPro; IPR002996; Cytkn recept_B/G.
InterPro; IPR003961; FN III.
InterPro; IPR003967; FN III.like.
InterPro; IPR003530; Hemptrecepti_F3.
InterPro; IPR003530; Hemptrecepti_F3.
InterPro; IPR003530; Hemptrecepti_F3.
InterPro; IPR003530; 1.
Pfam; PF00041; fn3; 1.
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DISULFID
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CARBOHYD
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174
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Alternative splicing; Direct protein sequencing;
Immunoglobulin domain; Receptor; Signal; Transmembrane.
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IG_LIKE; 1.
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Cytoplasmic (Potential).
Ig-like C2-type.
Fibromectin type-III.
WSXWS motif.
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N-linked (GlcNAc...
N-linked (GlcNAc...
N-linked (GlcNAc...
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Extracellular
                                                                                                                                                                                                                                                                                               signaling.
C->A: Comp
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                                                                                                                                                                                                                                                  signaling.
C->L: Comp
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D->T: 30% decrease c
                                                                                                                                                                                                                                                                      signaling.
                                                                                                                                                 u->v: Complete loss of ligand-binding R-SS: 30% decrease of ligand-binding
                                                                                                                                                                                 no IL6 signaling.
C->D: Complete loss of ligand-binding and
                                                                                                                                                                                                                                  signaling
                                                                                                                                                                                                                                           F->L: No
                                                                 100% increase in IL6 signaling.
V->N: 50% Decrease of ligand-binding a
U->D: Complete loss of ligand-binding.
I->D: Complete loss of ligand-binding and
                                                                                                                                                                              C->A: No change of
                                                                                                                                                                                                      IL6 signaling.
V->G: 80% decrease
                                                                                                                                      W->Q: 30% decrease of ligand-binding
                                                                                                                                               97.I
            no IL6 signaling.
Q->K: Complete loss
R->G: Complete loss
                                    no IL6 signaling.
G->D: 80% decrease
                                                                                                                                increase
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9
                                                                                                                                              signaling.
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                                                     signaling
G: 70% decrease
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D: 30% increase of ligand-binding
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018796;
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16-0CT-2001
05-JUL-2004
                                                             STRAND
TURN
                                                                                                                                                                 SEQUENCE OF 123-186
                                                                                                                                                                                   Submitted
                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                           Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                      Name=IL6R;
                                                                                                                                                      TISSUE=Liver;
                                                                                                                                                                                                      Morris K.R., Strom A.D.G.; "Cloning and expression of biologically
                                                                                                                                                                                                                                            NCBI_TaxID=9823;
                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                Interleukin-6
similarity).
SUBCELLULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: Expressed in liver.
DOMAIN: The two fibronectin type III-like domains
C-terminal part form together a cytokine-binding d
DOMAIN: The WSXWS motif appears to be necessary for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PEGDSSFYIVSMCVASSVGSKFSKTQTFQGCGILQPDPPANITVTAVARNPRWLSVTWQD
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                                                                                                                                                                                     (MAY-1999)
                                                                                                                                              Matteri R.L.;
                                                                                                                                                                                                                                                                                     (Rel. 40, Createu,
(Rel. 40, Last sequence update)
(Rel. 44, Last annotation update)
-6 receptor alpha chain precursor
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Cetartiodactyla; Suina;
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96.5%;
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1; Mismatches
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ina; Suidae; Sus.
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SIGNAL
CHAIN 2
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CARBOHYD
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InterPro; IPR007110; Ig-like.
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SIMILARITY: Belongs to the type I cytokine family osubfamily 3.
SIMILARITY: Contains 1 fibronectin type III domain.
SIMILARITY: Contains 1 immunoglobulin-like C2-type of the cantains 1 immunoglobulin-like C2-type of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             European Bioinformatics Institute.
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PF00047; ig; 1.

TE; PS50853; FN3; 1.

TE; PS01354; HEMATOPO REC L F3; 1.

TE; PS50835; IG LIKE; 1.
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AF015116; AAB70916.1;
P08887; 1N26.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                         VLRKPAAGSHPSRWAGMGRRLLLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPEEPQLS
GEWSEWSPEAMGTPWTESRSPPAENEVSTPMQALTTINKDDDNILFRDSANATSLPVEFMP
                                                                                                                      PHSWNSSFYRLRFELRYRAERSKTFTTWMVKDLQHHCVIHDAWSGLRHVVQLRAQEEFGQ
                                                                                                                                                                                                                                     PEGDSSFYIVSMCVASSVGSKFSKTQTFQGCGILQPDPPANITVTAVARNPRWLSVTWQD
                                                                                                                                                                                                                                                                                                                                                         CFRKSPLSNVVCEWGPRSTPSLTTKAVLLVRKFQNSPAEDFQEPCQYSQESQKFSCQLAV
                                                                                                                                                                                                                                                                                                             CFRKSPLSNVGCEWRPRSPPSPTTKAVLLVRKFQNSPVEDFQEPCQYSLEAQRFFCQLAV
                                                                                                                                                                                                                                                                                                                                                                                                                            VLRNQVTGSPDGRPAGVGRRLLLKSVQLSDSGNYSCYQDGVPAGSVRLLVDAPPEEPQLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MLAVGCALLTALLAAPGMALAPRGCSKLEVAQDVLTSLPGASVTLTCPGGEPGDNATIHW
                                                                                       PPSWNSYFYRLQFELRYRAERSKTFTTWMVKELQHHCIIHDAWSGMRHVVQLRAQEEFGH
                                                                                                                                                                                                  PEGDNSFHIVTLCVANSAGSQSSTPQTFEGYGILQPDPPVNITVSAVDRNPRWLSVTWQD
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IPR003961; FN_III.
IPR008957; FN_III-like.
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75.1%;
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Ig-like C2-type.

Fibronectin type-III.

WSXWS motif.

WS similarity.

By similarity.

By similarity.

By similarity.

By similarity.

N-linked (GlcNAc...

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Pred. No. 5
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.7e-95;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 467;
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P22273;
01-AUG-1991 (Rel. 19, C
01-FEB-1995 (Rel. 31, I
05-JUL-2004 (Rel. 44, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat)
Eukaryota; Metazoa; Cho:
Mammalia; Eutheria; Rode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Interleukin-6 receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=Fischer 344; TISSUE=Liver;
MEDLINE=91060602; PubMed=2174054;
Baumann H., Baumann H., Evy G.H.;
Molecular cloning, characterization
"Molecular cloning, characterization
"Molecular cloning, characterization
"Aller interleukin 6 receptor",
rat liver interleukin 6 receptor",
rat liver interleukin 6 receptor",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished observations (FEB-1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DENTIFICATION OF PROBABLE FRAMESHIFT
                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between the Swiss Institute of Bioinformatics and the EMBL outstation on its European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way use by non-profit institutions as long as its content is no moved. We and for commercial modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                          RGD;
                                                                                                                                                                                                                                                                                          EMBL; M58587; AAA41431.1; -. PIR; A37986; A37986. HSSP; P08887; IN26.
                                                                                                                                          InterPro; IPR002996; Cytkn recept_B/G.
InterPro; IPR003961; FN_III.
InterPro; IPR008957; FN_III-like.
InterPro; IPR003530; HemptreceptL_F3.
InterPro; IPR007110; Ig-like.
                                                                                                                                                                                                                                                RGD; 2902;
InterPro; I
                          PROSITE; PS50853; FN3; 1.
PROSITE; PS01354; HEMATOPO REC_L_F3;
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biol.
                                                                                                        Pfam; PF00041; fn3; Pfam; PF00047; ig;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: Part of the receptor for interleukin 6. Binds to II with low affinity, but does not transduce a signal. Signal activation necessitate an association with IL6ST. Activation lead to the regulation of the immune response, acute-phase reactions and hematopoiesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: Type I membrane protein.
SUBCELLULAR LOCATION: Type I membrane protein.
DOWAIN: The two fibronectin type III-like domains contained in the DOWAIN: The two fibronectin type III-like domains contained in the DOWAIN: The ways motif appears to be necessary for proper protein DOWAIN: The Ways motif appears to be necessary for proper protein folding and thereby efficient intracellular transport and cell-folding and thereby efficient intracellular transport.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBUNIT: Hexamer of two molecules each of IL6, IL6R and IL6ST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: Belongs to the type I cytokine family of Similarity: Belongs to the type I cytokine family of Similarity: Contains 1 fibronectin type III domain.
SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
SIMILARITY: Contains 1
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Chem. 265:19853-19862(1990).
                                                                                                                                                                                                                                                                                Il6r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
             Immunoglobulin
                                                                                                                                     fn3;
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Rodentia;
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Last annotation updat
or alpha chain precurso
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Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                        domain;
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                             Receptor;
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                                Signal;
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P22772;
01-AUG-1991 (Rel. 19, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
05-JUL-2004 (Rel. 44, Last annotation update)
Interleukin-6 receptor alpha chain precursor
Name=Il6ra; Synonym=Il6r;
SEQUENCE FROM N.A.
STRAIN-BALB/c; TISSUE=Spleen;
MEDLINE=90278354; PubMed=2112585;
MEDLINE=90278354; PubMed=2112585;
Sugita T., Totsuka T., Saito M.,
                                                                                                            Mus musculus (Mouse
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            194;
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Rodentia;
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By similarity.
N-linked (GlcNAc. .) (Potential).
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Cytoplasmic (Potential).
Ig-like C2-type.
Fibronectin type-III.
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Extracellular (Potential)
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Pred. No. 2.3e
51; Mismatches
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                                                                                                                        Craniata; Vertebrata;
Sciurognathi; Muridae;
                    Yamasaki
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                                                                                                                                    Muridae;
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: Murinae; Mus
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                                Hirano
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                                                                                                                                                                                                                         Glycoprotein;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                PIR; JL0144; JL0144.
PIR; JL0145; JL0145.
HSSP; P08887; 1N26.
                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X51975; CAA36237.1; -. EMBL; X53802; CAA37810.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN=C3H; TISSUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           particle gene product at its plasmacytomagenesis.";
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                    MGD; MGI:105304; Il6ra.
                                                                                                                                                                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                                                                                         interPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  surface receptor binding
- SIMILARITY: Belongs to t
Subfamily 3
- SIMILARITY: Contains 1 f
- SIMILARITY: Contains 1 i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Type I membrane protein.

DOMAIN: The two fibronectin type III-like domains contained in the C-terminal part form together a cytokine-binding domain.

DOMAIN: The WSXWS motif appears to be necessary for proper protein folding and thereby efficient intracellular transport and cell-surface receptor binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rillo M.T., Ciliberto G., Dente L.;
mitted (UUL-1990) to the EMBL/GenBank/DDBJ databases.
mitted(UUL-1990) to the receptor for interleukin 6. Binds to IL-6
with low affinity, but does not transduce a signal. Signal
activation necessitate an association with IL6ST. Activation may
lead to the regulation of the immune response, acute-phase
reactions and hematopoiesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 reactions and hematopoiesis.
SUBUNIT: Hexamer of two molecules each of IL6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      similarity).
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PS01354; HEMATOPO_REC_L_F3;
PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                            IPR002996; Cytkn recept B/G
IPR003961; FN IIT.
IPR008957; FN III-like.
IPR003530; HemptreceptL F3.
             TISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  171:2001-2009(1990).
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        WSXWS motif.

By similarity.

By similarity.

By similarity.

By similarity.

N-linked (GlcNAc...

                                                                                                                                           Ig-like
Fibronec
                                                                                                                                                                                                                                   domain; Receptor; Signal; Transmembrane.
                                                                                                                                                                      Cytoplasmic (Potential).
                                                                                                                                                                                 Potential
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                                                                                                                                         bronectin type-III.
                                                                                                                                                          C2-type
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CRC64;
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(Potential).
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MBL outstation -
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SIANDER STATE

P05231; O9UCU2; O9UCU3; O9UCU4;

13-AUG-1987 (Rel. 05, Created)

13-AUG-1987 (Rel. 05, Last sequence update)

01-OCT-2004 (Rel. 45, Last annotation update)

Interleukin-6 precursor (IL-6) (B-cell stimulatory)

(Threrferon beta-2) (Hybridoma growth factor) (CTL)
[3]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=87067433; PubMed=3538015;
May L.T., Helfgott D.C., Sehgal P.B.;
"Anti-beta-interferon antibodies inhibit the increased emanti-beta-interferon antibodies factor-treated human fibrostructural studies of the beta 2 interferon involved.";
structural studies of the beta 2 interferon involved.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE=87065033; PubMed=3491322;
Hirano T., Yasukawa K., Harada H., Taga T., Watan
Kashiwamura S.-I., Nakajima K., Koyama K., Iwamat
Sakiyama F., Mateui H., Takahara Y., Taniguchi T.
"Complementary DNA for a novel human interleukin
B lymphocytes to produce immunoglobulin.";
Nature 324:73-76(1986).
                                                                                                                                                                                                                                               EMBO
                                                                                                                                                                                                                                                                 "Structure and 2/IL-6) gene.";
                                                                                                                                                                                                                                                                                                                    Nakai S., Kishimoto
                                                                                                                                                                                                                                                                                                                                         MEDLINE-88082664; PubMed=3500852;
Yasukawa K., Hirano T., Watanabe Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia; Butheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
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Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121
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                                                                                                                                                                                                                                          gene.";
6:2939-2945(1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CFRKSPLSNVVCEWGPRSTPSLTTKAVLLVRKFQNSPAE-DFQEPCQYSQESQKFSCQLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VLRKPAAGSHPSRWAGMGRRLLLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPEEPQLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MLAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QGEWSEWSPEAMGTPW-TESRSPPAENEVSTPMQALTTNKDDDNILFRDSANATSLPVEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DPHSWNSSFYRLRFELRYRAERSKTFTTWMVKDLQHHCVIHDAWSGLRHVVQLRAQEEFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VPEGDSSFYIVSMCVASSVGSKFSKTQTFQGCGILQPDPPANITVTAVARNPRWLSVTWQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MLTVGCTLLVALLAAPAVALVLGSCRALEVANGTVTSLPGATVTLICPGKEAAGNVTIHW
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                                                                                                                                                                                                                                                                                      expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SGSQNREWTTTGNTLVLRDVQLSDTGDYLCSLNDHLVGTVPLLVDVPPEEPKLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50.1%;
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                                                                                                                                                                                                                                                                                        human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                           Ħ
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                                                                                                                                                                                                                                                                                           cell
                                                                                                                                                                                                                                                                                                                                         Muratani K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
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nes 122;
                                                                                                                                                                                                                                                                                           stimulatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Iwamatsu
Juchi T., K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Watanabe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BSF-2)
                                                                                                                                                                                                                                                                                                                                           Matsuda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               abe Y., Matsuda T
Bu A., Tsunasawa 
Kishimoto T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo
                                                                                                                                                                                                                                                                                           factor-2
                                                                                                                     expression
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             induces
                                                                                                                                                                                                                                                                                           (BSF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                     of.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      179
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, REPERT REPORTED BY A SERVICE 
RX Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
RA Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
RA Klausmer R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Bulterifield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

MEDLINE=87053818; PubMed=3023045;

Zilberstein A., Ruggieri R., Korn J.H., Revel M.;

"Structure and expression of cDNA and genes for human interferon-beta-
"Structure and expression of cDNA and genes for human interferon-beta-
2, a distinct species inducible by growth-stimulatory cytokines.";

EMBO J. 5:2529-2537(1986).
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J. Immunol. 139:4116-4121(1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brakenhoff J.P.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Molecular cloning and Escherichia coli.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Aarden L.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=88088768;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    stabilization of the mRNA cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tonouchi N., Miwa K., Karasuyama H., Mate Tonouchi N., Miwa K., Karasuyama H., Miwa K.,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=89391958;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
TISSUE-Fibroblast;
MEDLINE-87004683; Pubmed-3758081;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Structural analysis of the sequence protein in human fibroblasts.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

MEDLINE=89193317; PubMed=3266463;
MONG G., Witek-Giannotti J., Hewick
Wong G., Witek-Giannotti J. at a a
"Interleukin 6: identification as a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fiers W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Haegeman G., Content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mammalian cells after
Chung-Hua Chung Liu Te
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nickerson D.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Stable and efficient expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=93178270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rieder M.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM
TISSUE=Lung;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "SeattleSNPs. NHLBI
FHCRC, Seattle, WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (JUN-2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Carrington D.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=3320204;
, de Groot E.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    159:625-632(1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=2789513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=1291290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83:40-47(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       URL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tsa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AND VARIANTS SER-32 gton D.P., Chung M.-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HL66682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    expression
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene transfer.";
sa Chih 14:340-344(1992)
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MEDLINE=88154445;
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"Evidence for the importance of a positive charge

structure of the C-terminus for biological activit

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by NMR spectroscopy.";
Biochemistry 35:273-281(1996).
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Cumming D.
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Nishimura C., Watanabe A., Gouda H.,
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  "1.9-A crystal structure of interleukin 6: i

"1.9-A crystal structure of interleukin 6: i

mode of receptor dimerization and signaling

EMBO J. 16:989-997(1997).

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-1- FUNCTION: IL-6 is a cytokine with a wide

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RA Hillier L.W., Sekhon M., Becker M.C., O'Laughlin M.D., Schaller M.E.,
RA Wylie K., Sekhon M., Becker M.C., O'Laughlin M.D., Schaller M.E.,
RA Fewell G.A., Delehaunty K.D., Miner T.L., Nash W.E., Cordes M., Du H.,
RA Sun H., Edwards J., Bradshaw-Cordum H., Ali J., Andrews S., Isak A.,
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RA Ozersky P., Miller N., Johnson C., Dauphin-Kohlberg S.,
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RA Hickenbotham M.T., Eldred J., Williams D., Bedell J.A., Mardis E.R.,
RA Clifton S.W., Chissoe S.L., Marra M.A., Raymond C., Haugen E.,
RA Gillett W., Zhou Y., James R., Phelps K., Iadanoto S., Bubb K.,
RA Baertsch R.A., Brent M.R., Keibler E., Flicek P., Bork P., Suyama M.,
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SUBCELLULAR LOCATION: Secreted.

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SIMILARITY: Belongs to the IL-6 superfamily.

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Primates;
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97.9%;
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Last annotation updat
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Mismatches
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Best Local Similarity
Matches 187; Conserv
    Matches
                           Query Match
Best Local :
                                                                                                            SEQUENCE FROM N.A.

Ebert L., Schick M., Neubert P., Schat

"Cloning of human full open reading fi

"cloning of human full open reading fi

vector (pDONR201).";

vector (pDONR201).";

charted (MAY-2004) to the EMBL/GenBe

EMBL; CR450296; CAG2992.1;

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                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Ch
Mammalia; Eutheria; Pa
NCBI_TaxID=9606;
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Submitted
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Submitted
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"The DNA sequence of human chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein. SEQUENCE 212 AA; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (JAN-2004) to the EMBL; AC073072; AAS07539.1;
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                                                                                            SEQUENCE
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20-MAY-2004
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Submitted (JUN-2000)
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    187;
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                           Similarity
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(SEP-2001)
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                                                                                          212 AA;
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of Homo sapiens BAC clone RP11-240H8.";
N-2000) to the EMBL/GenBank/DDBJ databas
                                                                                                                                                                                                                                                                                                         Chordata;
Primates;
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Pred. No. 4e-5
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                           Score 938.5;
Pred. No. 4e-
                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                           4e-58;
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Gateway (TM)
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P79341;
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation updat
7nterleukin-6 precursor (IL-6)
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IL6_MACFA
                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases -i- FUNCTION: IL-6 is a cytokine with a wide variety of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Molecular cloning 6.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                        PRINTS; PRO0433; ILGGCSFMGF.
PRINTS; PR00434; INTERLEUKIN6.
PRODOM; PD004356; Interleukin_6;
SMART; SM00126; IL6; 1.
PROSITE; PS00254; INTERLEUKIN_6;
                                                                                                                                                                                       InterPro; IPR009079; 4 helix cytokine.
InterPro; IPR003573; II6_MGF_GCSF.
InterPro; IPR003574; Interleukin_6.
Pfam; PF00489; IL6; 1.
                                                                                                                                                                                                                                                     EMBL;
                                                DISULFID
DISULFID
CARBOHYD
                                                                                      SIGNAL
                                                                                                                                                                                                                                           HSSP;
                                                                                                                  Acute
                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: IL-6 is a cytokine with a wide variety of biological functions; it plays an essential role in the final differentiation of B-cells into Ig-secreting cells, it induces myeloma and plasmacytoma growth, it induces nerve cells differentiation, in hepatocytes it induces acute phase reactants (By similarity). SUBCELLULAR LOCATION: Secreted.

SUBCELLULAR LOCATION: Secreted.
SIMILARITY: Belongs to the IL-6 superfamily.
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                                                                                                                                                                                                                                           P05231; 1IL6
                                                                                                               phase;
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                           30
72
101
73
172
212
                                          ; Cytokine; (29) 1 29 30 212 78 78 111 111 73 73 172 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                             AΑ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and expression of cynomolgus monkey interleukin-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             543
                                                                                                                                 INTERLEUKIN_6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      212
                                        e; Glycoprotein; Growth factor; S:
29 By similarity.
21 Interleukin-6.
22 By similarity.
23 By similarity.
24 N-linked (GlCNAc. . . ) (1)
25 N-linked (GlCNAc. . . ) (1)
                                23654
      31.7%;
                                 ¥.
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         Score
                               CF8173FCBF0B0389
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         907.5;
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            BB
            ۲.
                                      CRC64;
            Length
                                                (potential). (potential).
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THE REAL BRIDGE SECOND 
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P51494;
01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence up
05-UUL-2004 (Rel. 44, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cercopithecinae; Macaca.
NCBI_TaxID=9544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Macaca mulatta (Rhesus macaque)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Interleukin-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=96003435; PubMed=7561102;
Villinger F.J., Brar S.S., Mayne A.E., Chil
"Comparative sequence analysis of cytokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN=RAC 2;
                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial modifies requires a license agreement (See http://www.isb-sib.ch/announce/entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Immunol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nonhuman primates."
                                                                                                                                                                                                                               EMBL; L26028; AAA99978.1; --
HSSP; P05231; IALU.
InterPro; IPR009079; 4 helix cytokine.
InterPro; IPR003573; II6 MGF_GCSF.
InterPro; IPR003574; Interleukin_6.
                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement or send an email to license@isb-sib.ch
                                                                                                                                   PRINTS; PR00433; ILGGCSFMGF.
PRINTS; PR00434; INTERLEUKING.
PRODOM; PD004356; Interleukin
                                                                                           SMART; SM00126; II
PROSITE; PS00254;
                           SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: II-6 is a cytokine with a wide variety of biologica functions: it plays an essential role in the final differential of B-cells into Ig-secreting cells, it induces myeloma and plasmacytoma growth, it induces nerve cells differentiation, plasmacytoma growth, it induces nerve cells differentiation, plasmacytose it induces acute phase reactants (By similarity). SUBCELLULAR LOCATION: Secreted.
SUBCELLULAR LOCATION: Secreted.
SIMILARITY: Belongs to the II-6 superfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              354 LPVEF-MPVPPGEDSKDVAAPHROPLTSSBRIDKQIRYILDGISALRKETCNKSNMCESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        142
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                                                                                                                                                                                                                PF00489; IL6;
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                                                                                                                      SM00126;
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                                                                                                                                                                                                                                                                                                                                                                            email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                precursor (IL-6).
                                                                     0254; INTERLEUKIN_6; 1.
Cytokine; Glycoprotein;
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                                                                                                                                               Interleukin_6;
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3; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi; Catarrhini; Cercopithecidae;
              By similarity.
Interleukin-6.
By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       update)
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                                                                                      Growth
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kine genes from human
                                                                                              factor;
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097540; Ol-MAY-1999 (TrEMBLrel. 10,
01-MAY-1999 (TrEMBLrel. 10,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Identification, cloning, and sequencing of different in four species of owl monkey.";
Immunogenetics 54:645-653 (2002).

EMBL; AF014510; AAD01536.1; -.
GO; GO:0005576; C:extracellular; IEA.
GO; GO:0005125; F:cyrcokine activity; IEA.
GO; GO:0005125; F:interleukin-6 receptor binding; IEA.
GO; GO:0005538; F:interleukin-6 receptor binding; IEA.
TOTATOTO. 1 TEBERGATO. 1
                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PRO0433; ILGGCSFMGF.
PRINTS; PR00434; INTERLEUKIN6.
ProDom; PD004356; Interleukin 6; 1.
SMART; SM00126; IL6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Aotus nancymaae (Ma's night monkey).
Eukaryota; Metazoa; Chordata; Craniata; Ve;
Mammalia; Eutheria; Primates; Platyrrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=IL-6;
                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00254; INTERLEUKIN_6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00489; IL6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR009079; 4 helix cytokine.
InterPro; IPR003573; IL6 MGF GCSF.
InterPro; IPR003574; Interleukin_6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Murillo L.A., Patarroyo M.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=22354194; PubMed=12466897;
Hernandez E.C., Suarez C.F., Mende
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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N-inked (GlcNAc. ..) (Potential)
N-linked (GlcNAc. ..) (Potential)
1 (BlcNAc ...) (Potential)
1 (Algorithm of the control of t
                                                                                                                        Score 898.5; DB 2;
Pred. No. 2.6e-55;
5; Mismatches 4;
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Pred. No. 2.2e-5
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ni; Cebidae;
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outset the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. Immunol. 155:3946-3954 (1995).

-!- FUNCTION: IL-6 is a cytokine with a wide variety of biologics functions: it plays an essential role in the final differenti of B-cells into Ig-secreting cells, it induces myeloma and plasmacytoma growth, it induces nerve cells differentiation, hepatocytes it induces acute phase reactants.

-!- SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=96003435; PubMed=7561102;
Villinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;
"Comparative sequence analysis of cytokine genes from human and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cercocebus torquatus atys (Red-crowned mangabey) (Sooty mangabey). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P46650;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                PRINTS; PR00433; IL6GCSFMGF.
PRINTS; PR00434; INTERLEUKIN6.
PYCDOM; PD004356; Interleukin
SMART; SM00126; IL6; 1.
                                                                                                                                                                                                                             SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                        Ptam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nonhuman
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                                                                                                                                                                                                                                                    Acute phase; Cytokine;
                                                                                                                                                                                                                                                                              PROSITE; PS00254;
                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR003574; Interleukin 6.
Pfam; PF00489; IL6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR009079; 4_helix_cytokine.
InterPro; IPR003573; IL6_MGF_GCSF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: Belongs to the IL-6 superfamily.
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11 Interleukin-6.
18 By similarity.
11 By similarity.
11 By similarity.
11 N-linked (GloNAc....
73 N-linked (GloNAc....
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Pred.
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EMBL; AF294757; AAK92044.1; -.

MR HSSP; D95231; IIL6.

GO; GO:0005576; C:extracellular; IEA.

GO; GO:0005125; F:cytokine activity; IEA.

GO; GO:0005128; F:interleukin-6 receptor binding; IEA.

GO; GO:0005128; F:interleukin-cresponse; IEA.

R GO; GO:0005128; F:interleukin-6.

R GO; GO:0005128; F:interleukin-6.

R GO; GO:0005128; F:interleukin-6.

R InterPro; IPR003573; II6_MGF_GCSF.

R InterPro; IPR003574; Interleukin-6.

R Pfam; PF00389; II6; I.

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01-MAR-2004
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Saimiri sciureus (Common squirrel monkey).
Saimiri sciureus (Common squirrel monkey).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Platyrrhini; Cebidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q8MKH0;
                                                                                                                                                                                                                                                                                                                                 Heraud J.M., Lavergne A., Kazanji M.; "Molecular cloning, characterization, a monkey ( Saimiri sciureus) Th1 and Th2
                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21972723; PubMed=11976788;
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9521;
                                                                                                                                                                       PRINTS; PR00434; INTERLEUKIN6.
PRINTS; PR00434; INTERLEUKIN6.
ProDom; PD004356; Interleukin_6; 1.
SMART; SM00126; IL6; 1.
SNORTE; PS00254; INTERLEUKIN_6; 1.
PROSITE; PS00254; INTERLEUKIN_6; 1.
SEQUENCE 212 AA; 23581 MW; FF22CBF493245479 CRC64;
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Cebinae; Saimiri.
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01-MAY-2000 (TremBLrel
01-MAR-2004 (TremBLrel
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Platyrrhini; Cebidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE=22354194; PubMed=12466897;

Hernandez E.C., Suarez C.F., Mendez J.A.,

Hernandez E.C., Suarez M.B.;

Hernandez E.C., Patarroyo M.B.;

Annillo L.A., Patarroyo M.B.;
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     01-MAY-2000 (TrEMBLrel. 13, C
01-MAY-2000 (TrEMBLrel. 13, L
01-MAR-2004 (TrEMBLrel. 26, La
Interleukin-6 (Fragment).
Name-IL-6;
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Q9TTH4;
01-MAY-2000
01-MAY-2000
01-MAR-2004
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209 AA;
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                                                                                                                            PRELIMINARY;
         (Black-headed
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23115 MW; A0A3DFAA4BF560CC CRC64;
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on update)
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Best Local
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                 Youn H. Y., Shin I.-S.;
Submitted (JUN-2000) to the EMBL/GenBank/DDI
Submitted (JUN-2000) to the EMBL/GenBank/DDI
EMBL; AP275796; AAF86275.1; -.
HSSP; P05231; IIL6.
GO; GO:0005135; F:cytrokine activity; IEA.
GO; GO:0005135; F:interleukin-6 receptor bi:
GO; GO:0005135; F:interleukin-6 receptor bi:
GO; GO:0005135; F:interleukin-6 receptor bi:
GO; GO:0005135; F:interleukin-6.
InterPro; IPR003573; ITE_MGF_GCSF.
InterPro; IPR003574; Interleukin-6.
Pfam; PF00489; IL6; 1.
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01-OCT-2000
01-MAR-2004
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                                                                                                                                                                                                                                                                                                                                                                                               Canis familiaris (Dog).
Canis familiaris (Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00489; IL6; 1.

PRINTS; PR00433; IL6GCSFMGF.

PRINTS; PR00434; INTERLBUKIN6.

ProDom; PD004356; Interleukin 6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunogenetics 54:645-653(2002).

EMBL, AF097322; AAR21297.1; -.

GO, GO:0005556; C:extracellular; IEA.

GO; GO:0005125; F:cytokine activity; IEA.

GO; GO:0005138; F:interleukin-6 receptor binding; IEA.

GO; GO:0006955; P:immune response; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=22354194; PubMed=12466897;
Hernandez E.C., Suarez C.F., Mende
Murillo L.A., Patarroyo M.E.;
                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=IL-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00254; INTERLEUKIN_6; 1.
NON_TER 1 1
SEQUENCE 175 AA; 19205 MW; 2BCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Identification, cloning, and sequencing in four species of owl monkey.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QEALAENNLNLPKMAEKDGCFQSGFNEETCLLKITTGLLEFEVYLEYLQNRFESSKEQAG
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    IL6GCSFMGF
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RESULT 16

II.6 PROVIDE AC Q288

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Best Local S
Matches 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Molecular cloning and sequencing of interleukin 6 cDNA fragments the harbor seal (phoca vitulina), killer whale (Orcinus orca), are Southern sea otter (Enhydra lutris nereis).";

Immunogenetics 43:190-195(1996).

-I- FUNCTION: IL-6 is a cytokine with a wide variety of biological functions: it plays an essential role in the final differentiation of B-cells into Ig-secreting cells, it induces myeloma and plasmacytoma growth, it induces nerve cells differentiation, hepatocytes it induces acute phase reactants (By similarity).

-I- SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IL6_PHOVI STANDARD, PRT, 209 AA. (208819)
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ProDom; PD004356; Interleukin_6; 1.
SMART; SM00126; IL6; 1.
PROSITE; PS00254; INTERLEUKIN 6; 1.
SEQUENCE 207 AA; 23042 MW; 4554
                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outset the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/ar
                                                                                                                                                             EMBL; L46802;
HSSP; P05231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stott J.L., Ferrick D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ring
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Pinnipedia; Phocidae; Phoca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Phoca vitulina (Harbor seal).
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                                                                                                                                                                                                                                             send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: Belongs to the IL-6 superfamily.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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Pfam; PF00489; II PRINTS; PR00433; PRINTS; PR00434;

IL6;

INTERLEUKIN6 IL6GCSFMGF InterPro; IPR009079; 4 helix_cytokine InterPro; IPR003573; IL6_MGF_GCSF. InterPro; IPR003574; Interleukin_6.

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SQ FT FT ST
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SEQUENCE
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                                                                                                                                                                                Leutenegger C.M., Huder in Molecular cloning of equipmonitted (JUL-1997) to t [3]
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Q95181; 019007; 046568;
Q95181; 019007; 046568;
Created)
O1-NOV-1997 (Rel. 35, Created)
O5-UUL-1999 (Rel. 38, Last sequence up
O5-UUL-2004 (Rel. 44, Last annotation
Interleukin-6 precursor (IL-6).
                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus
                                                                                                                                                                                                                                                                            MEDLINE=20579380; PubMed=11137120;
Swiderski C.E., Sobol G., Lunn D.P.,
Swiderski C.E., Sobol G., Lunn D.P.,
"Molecular cloning, sequencing, and (
                                                                                                                                                         SEQUENCE FRO
                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                             "Cloning and expression of equine interleukin-6.";
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.

Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.

1- FUNCTION: It-6 is a cytokine with a wide variety of biological functions: it plays an essential role in the final differentiation of B-cells into Ig-secreting cells, it induces myeloma and of B-cells into Ig-secreting cells, it induces myeloma and plasmacytoma growth, it induces nerve cells differentiation, in hepatocytes it induces acute phase reactants (By similarity).

hepatocytes it induces acute phase reactants (By similarity).

-i- SUBCELLULAR LOCATION: Secreted.

-i- SUBCELLULAR LOCATION: Secreted.
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; SM00126; IL
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PS00254; INT
  SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
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ProDom; PD004356; Interleukin_6;
SMART; SM00126; IL6; 1.
PROSITE; PS00754
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use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
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InterPro; IPR003573; II6 MGF_GCSF.
InterPro; IPR003574; Interleukin_6.
Pfam; PF00489; II6; 1.
PRINTS; PR00433; IL6GCSFMGF.
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EMBL; AF005227; AAB62246.1; ---
EMBL; AF041975; AAC04574.1; ---
EMBL; T09216; T09216.
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30-MAY-2000 (R
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SEQUENCE FROM N.A.
MEDLINE=96163018; PubMed=8575817;
MEDLINE=96163018; PubMed=8575817;
Ming D.P., Schrenzel M.D., McKnight
King D.P., Schrenzel M.D.A.;
Stott J.L., Ferrick D.A.;
"Molecular cloning and sequencing of
                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
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Cetartiodactyla; Cetacea; Odontoceti; Delphin
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InterPro; IPR003573; IL6_MGF_GCSF.
InterPro; IPR003574; Interleukin_6.
Pfam; PF00489; IL6; 1.
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                         Interleukin 6.
Delphinapterus leucas (Beluga whale).
Bukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalla, Eutheria, Cetartiodactyla, Cetacea; Odontoceti;
Monodontidae, Delphinapterus.
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01-NOV-1999 (TrEMBLrel.
01-NOV-1999 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Immunogenetics 43:190-195(1996).

-IF-FUNCTION: IL-6 is a cytchkine with a wide variety of biological functions: it plays an essential role in the final differential of B-cells into Ig-secreting cells, it induces myeloma and plasmacytoma growth, it induces nerve cells differentiation, heparcocytes it induces acute phase reactants (By similarity).

SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Southern sea otter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: Belongs to the IL-6 superfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72
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|||:|:| | | |::| || | :|| || |::| |||||
IEAVQISSKALAQILRQKVKNPDEVTTPDPTTNASLMNNLQSQNDDMMKNTKIILILRSL 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seal (Phoca vitulina),
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                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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Interleukin-6.
By similarity.
By similarity.
N-linked (GlCNAC.
                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                    Created)
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Pred. No. 3e-32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  There are no restrictions on ong as its content is in no oved. Usage by and for commen
                                                                                                                                                                                                                                                                                                                                                      ₽
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RESULT 20
IL6_CANFA
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Best Local Sim
Matches 113;
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SEQUENCE FROM N.A.

MEDLINE=20141864; PubMed=10678396;

MEDLINE=20141864; PubMed=10678396;

St-Laurent G., Archambault D.;

"Molecular cloning, phylogenetic analysis and experiments (Delphinapterus leucas) interleukin 6.";

whale (Delphinapterus leucas) interleukin 6.";

vet. Immunol. Immunopathol. 73:31-44(2000).

EMBL; AF076643; AAD42929.1; -...

HSSP; P05231; 1ADU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Interpro; IPR00979; 4 helix cytokine.
Interpro; IPR003573; II_MGF_GCSF.
Interpro; IPR003574; Interleukin_6.
Pfam; PF00489; II6; 1.
PRINTS; PR00433; IL6GCSEMGF.
PRINTS; PR00434; INTERLEUKIN 6.
PRODOm; PD004356; Interleukin_6; 1.
SMART; SM00126; IL6; 1.
PROSITE; PS00254; INTERLEUKIN 6; 1.
PROSITE; PS00254; INTERLEUKIN 6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8888
                                                                                                           STRAIN=Mongrel;
MEDLINE=94303924; PubMed=7913298;
MEDLINE=94303924; PubMed=7913298;
Kukielka G.L., Youker K.A., Hawkins H.K.,
Ballantyne C.M., Smith C.W., Entman M.L.;
"Regulation of ICAM-1 and IL-6 in myocard:
                                                                                                                                                                                                                                                                                                          P41323;
01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence up
05-JUL-2004 (Rel. 44, Last annotation
                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; C
Mammalia; Eutheria; Carnivora;
MCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                         SEQUENCE FROM
                                                                                                                                                                                                                                                               Canis familiaris (Dog)
                                                                                                                                                                                                                                                                                               Interleukin-6
                                                                                                  reperfusion.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO:0005576; C:extracellular; IEA.
GO:0005125; P:cytokine activity; IEA.
GO:0005128; F:interleukin-6 receptor
GO:000518; P:immune response; IEA.
                                                                                                                                                                                                                                                                                                                                                                     CANFA
          N. Y. Acad. Sci. 723:258-270(1994).

FUNCTION: IL-6 is a cytokine with a wide variety of biological functions: it plays an essential role in the final difference of the surface of B-cells into Ig-secreting cells, it induces myeloma and plasmacytoma growth, it induces nerve cells differentiation hepatocytes it induces acute phase reactants.
 SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                               195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             208 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                        N.A.
                                                                                                                                                                                                                                                                                             precursor (IL-6).
                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PGPLGEDFKDDTTSDRLLLTSPDKTEALIKYILGKISAMRKEMCEKYDKCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23456 MW;
                                                                                                                                                                                                                                                    Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 562; DB 2;
Pred. No. 1.3e-31;
                                                                                                                                                                                                                                    Fissipedia; Canidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81CC85C6E80389C4
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                                                                                                                 myocardial ischemia:
                           nerve cells differentiation,
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                                                                                                                                             Perrard J.L.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 208;
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Canis.
                                                                        of biological
                                                       differentiation
                                                                                                                   effect
                                                                                                                                                Michael L.H.,
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                                                                                                                                                                                                            RESULT 21
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between the Single Institute. There are no restrictions on its the by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U12234; AAA83030.1; -. HSSP; P05231; 1IL6.
                                                                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PRO0433; IL6GCSPMGF.
PRINTS; PR00434; INTERLEUKIN6.
PTCDOm; PD004356; Interleukin_6; 1.
SMART; SM00126; IL6; 1.
PROSITE; PS00254; INTERLEUKIN_6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR009079; 4 helix cytokine.
InterPro; IPR003573; II6 MGF GCSF.
InterPro; IPR003574; Interleukin 6.
Pfam; PF00489; IL6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIGNAL
CHAIN
                                                                                                                                                                         IL6_LAMGL
Q865X6;
29-MAR-2004
29-MAR-2004
05-JUL-2004 (I
Interleukin-6
                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                 Lama glama (Llama).
                                                                            Raadan
                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                  391
                                                                                                                                                                                                                                                                                                                                                                                                         al Similarity
114; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             phase;
                                                                                                                                                                                                                                                       175
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                                                                                                                                                                                                                                                                     QAQNQWLQDMTTHLILRSFKEFLQSSLRALROM 543
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                                                                                                                                                                                                                                                                                                         LEPEVYLEYLONRFESSEROARAVOMSTKVLIOFLOKKAKULDAITTPDPTTINASLLTKL
                                                                                                                                                                                                                                                    QSQDECVKHTTIHLILRSLEDFLQFSLRAVRIM
                                                                             FROM N.A.
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67
96
207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cytokine; Glycoprotein;
                                                                                                                                                                 (Rel. 43, Created)
(Rel. 43, Last sequence update)
(Rel. 44, Last annotation update)
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                                                                                                                                                        precursor (IL-6).
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73
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22945 MW;
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                                                                               Yoshida R.,
                                                                                                                    Chordata; Craniata; Vertebrata; Euteleostomi;
Cetartiodactyla; Tylopoda; Camelidae; Lama.
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Pred.
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By similarity.
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No. 1
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                                                                                   Ohashi
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RESULT 22
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Matches 109
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way use by non-profit institutions as long as its content is in no way use by non-profit institutions as long as its content is in no way use by non-profit institutions as long as its content is in no way use by non-profit institutions as long as its content is in out removed. Usage by and for commercial modified and this statement is not removed. Usage by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the IL-6 superfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR009079; 4 helix cytokine.
InterPro; IPR003573; II6 MGF GCSF.
InterPro; IPR003574; Interleukin_6.
Pfam; PF00489; IL6; 1.
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PROSITE; PS00254; INTERLEUKIN_6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ProDom; PD004356; Interleukin_6;
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PRINTS; PR00434; INTERLEUKIN6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                 Q865W7;
01-JUN-2003
01-JUN-2003
01-MAR-2004
                                                                                                                                                                                                                                                  Q865W7
                                                                                                                                   Camelus bactrianus (Bactrian camel).
Camelus bactrianus (Bactrian camel).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus
                                               Onuma M.;
Submitted (APR-2003)
EMBL; AB107656; BAC7
                                                                                                                     NCBI_TaxID=9837;
                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
HSSP;
GO; GO
GO; GO
                                                                                                                                                                                      Interleukin
                                                                                               SEQUENCE FROM N.A.
                                                                                      Raadan
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L; AB107656; BAC75393.1; -.
P; P05231; 1II6.
G0:0005576; C:extracellular; IEA.
G0:0005125; F:cytckine activity; IEA.
G0:0005138; F:interleukin-6 receptor binding;
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DFLQFSLRAVRIM
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211 AA;
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                                                                                       Lee
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77 B:
110 B:
; 23988 MW;
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56.5%;
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24, Last sequence up
26, Last annotation
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Pred. No. 2.5e
35; Mismatches
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By similarity.
Interleukin-6.
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By similarity.
; BB82D263F0996B16
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                                                                 EMBL/GenBank/DDBJ
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                                                                                              Ohashi K.,
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InterPro; InterPro;

GO:0006955; P:immune

response; IEA.

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Best Local S
Matches 110
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PRINTS; PR0043; ILGGCSPMGF.

PRINTS; PR00435; INTERLEUKIN6.

ProDom; PD004356; Interleukin_6; 1

SMART; SM00126; IL6; 1.

PROSITE; PS00254; INTERLEUKIN 6; 1

SEQUENCE 211 AA; 23929 MW; ODE
                                                                                                                                                                                                                                                                                                                                                                                                                       116_PIG STANDARD,
P26893; Q95KN6;
01-AUG-1992 (Rel. 23, Created)
28-FEB-2003 (Rel. 41, Last sequence upono-
05-UUL-2004 (Rel. 44, Last annotation
05-UUL-2004 (Rel. 44, Last annotation)
                                                                                      STRAIN-Landrace x Meishan; TISSUE-Blood;
Liu S., Meng M., Gao R.;
"Cloning and expression of interleukin 6 gene from Landrance hybrid swine.";
           Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: IL-6 is a cytokine with a wide variety of biological functions: it plays an essential ein the final differentiation of B-cells into Ig-secreting cells, it induces myeloma and plasmacytoma growth, it induces nerve cells differentiation, in hepatocytes it induces acute phase reactants.
                                                                                                                                                                       Mathialagan N., Bixby J.A., Roberts M.R. "Expression of interleukin-6 in porcine, preimplantation conceptuses."; Mol. Reprod. Dev. 32:324-330(1992).
                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                 Richards C., Saklatvala J.;
"Molecular cloning and sequence of porcine expression of mRNA in synovial fibroblasts
                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=91338547; PubMed=1873476;
                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                      Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                    Name=IL6
                                                                                                                                                                                                                             MEDLINE=92360284; PubMed=1497880;
                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                    Cytokine 3:269-276(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   / Match 19.5%;
Local Similarity 57.0%;
hes 110; Conservative 3:
    SUBCELLULAR LOCATION: Secreted
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IPR003573; IL6 MGF GCSF.
IPR003574; Interleukin_6.
                                                                                                                                                                                                                                                                                                                                                                           Cetartiodactyla;
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Pred. No. 2.5e
34; Mismatches
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actyla; Suina; Suidae;
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in vitro.";
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Matches 111
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InterPro; IPR003573; II6 MGF GCSF.
InterPro; IPR003574; Interleukin_6.
Pfam; PF00489; II6; 1.
PRINTS; PR00433; II6GCSFMGF.
PRINTS; PR00434; INTERLEUKIN6.
PRODOm; PD004356; Interleukin_6; 1.
SMART; SM00206; II6; 1.
                                                                                                                                             Q8MJ75
Q8MJ75;
01-OCT-2002
01-OCT-2002
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CONFLICT
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SEQUENCE FROM N.A.
Lee D., Yoo H., Choi I.;
Submitted (JUN-2002) to the EMBL,
EMBL; AF518322; AAM74938.1; -.
HSSP; P05231; 1ALU.
GO; GO:0005576; C:extracellular;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00254; INTERLEUKIN_6; 1.
Acute phase; Cytokine; Glycoproteir
SIGNAL 1 29 By sin
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EMBL; M80258; AAC27127.1; -.
EMBL; AF309651; AAG27730.1; -.
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                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                              Sus scrofa
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PIR; I46621; I46621.
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                                                                           CBI_TaxID=9823;
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                                                                                                                                                                                                                                   DFLQFSLRAIRIM 212
                                                                                                                                                                                                                                                                                                      ARAVOMSTKVLIOFLOKKAKULDAITTPDPTTNASLLTKLQAQUQWLQDMTTHLILRSFK
                                                                                                                                                                                                                                                     EFLOSSLRALROM 543
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72
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101
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212 AA;
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AAC27127.1; -.
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212
78
111
30
23952
                                                                                        Chordata; Craniata; Vertebrata; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                  19.5%;
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Last anno
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Interleukin-6.
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E -> G (in Ref.
                                   EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 557.5;
Pred. No. 2.8
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                                   databases
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                                                                                         Euteleostomi;
Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Signal
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R InterPro; IPR009079; 4 helix cytokine.

R InterPro; IPR003574; Interleukin_6.

R InterPro; IPR003574; Interleukin_6.

R Pflam; PF00489; II6; 1.

R PFINTS; PR00433; INTERLEUKIN6.

R PRINTS; PR00434; INTERLEUKIN6.

R PRINTS; PR00435; Interleukin_6; 1.

R PRODOM; PD004356; Interleukin_6; 1.

R SMART; SM00126; INTERLEUKIN_6; 1.

R SMART; SM00126; INTERLEUKIN_6; 1.

SEQUENCE 212 AA; 23881 MW; IF540E7030BCFD77 CRC64;

SEQUENCE 212 AA; 23881 MW; IF540E7030BCFD77 CRC64;
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Best Local S
Matches 111
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01-NOV-1995 (R
01-NOV-1995 (R
05-JUL-2004 (R
Interleukin-6
                                                                                                                                                                                                                                                                           Felis silvestris catus (Cat).
Felis silvestris catus (Cat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae;
                                                                                                                                                                                                                                                                                                                                                                      PTI
97I
                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                             NCBI_TaxID=9685;
                                                                                                                                                                                                                                                                                                          Name=IL6
                                                                                                                                                                                                  Hasegawa A.; "Molecular cloning
                                                                                                                                                                                                                       Ohashi T., Matsumoto
                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE=94162386;
                                                                                                                                                         SEQUENCE FROM N.A. TISSUE-Lymphocytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO:0005125; F:cytokine activity; IEA.
GO:0005138; F:interleukin-6 receptor binding; IEA.
GO:0006955; P:immune response; IEA.
                                                                                                                         MEDLINE=94052249; PubMed=8234373;
Bradley W.G., Gibbs C., Kraus L., Good F
WMOlecular cloning and characterization
                                                                                                                interleukin-6.";
            This
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||:| || || ||:| | : : : |:||| |||:|:| | |
                             DC. SEXD. Biol. Med. 204:301-305(1993).

FUNCTION: IL-6 is a cytokine with a wide variety of biological functions: it plays an essential role in the final differentiation of B-cells into Ig-secreting cells, it induces myeloma and plasmacytoma growth, it induces nerve cells differentiation, in hepatocytes it induces acute phase reactants.

SUBCELLULAR LOCATION: Secreted.

SIMILARITY: Belongs to the IL-6 superfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      468
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een the Swiss In
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(Rel. 32, Last sequence up
(Rel. 44, Last annotation
                                                                                                                                                                                            Sci.
                                                                                                                                                                                                                                                                                                                    precursor (IL-6).
                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                        PubMed=8117820;
oto Y., Watari T.,
                                                                                                                                                                                           g of feline interleukin-6
55:941-944(1993).
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       Institute
                                                                                                                                                                                                                                                                                                                                                    Created)
    is copyright. It is produced through a collaboration stitute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  543
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pred. No. 3.8e
33; Mismatches
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zation of a
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                                                                                                                                                                                                                               Goitsuka R.,
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3.8e-31;
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cDNA encoding
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Felis.
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Matches 107
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097535
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the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb-or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; L16914; AAA16620.1; --
EMBL; D13227; BAA02507.1; --
EMBL; 146084; 146084.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00489; IL6; 1.
Pfam; PF00439; IKGGCSFMGF.
PRINTS; PR00433; INTERLEUKIN6.
PRINTS; PR00434; INTERLEUKIN6.
ProDom; PD004356; Interleukin.
SMART; SM00126; IL6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR009079; 4 helix_cytokine.
InterPro; IPR003573; II6_MGF_GCSF.
InterPro; IPR003574; Interleukin_6.
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Acute phase; Cytokine; Glycoprote
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                                                                                                                                               097535 PRELIMINAKY;
097535; (TrEMBLrel. 10, C
01-MAY-1999 (TrEMBLrel. 10, L
01-MAR-2004 (TrEMBLrel. 26, L
01-MAR-2004 (Fragment).
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SEQUENCE FROM N.A.

MEDLINE=22354194; PubMed=12466897;
Medinez E.C., Suarez C.F., Mendez
Murillo L.A., Patarroyo M.E.;
Murillo L.A., Patarroyo M.E.;
"Identification, cloning, and sequen
"Identification, cloning, and sequen
                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=57176;
                                                                                                  Aotus vociferans (Spix's owl monkey).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Platyrrhini; Cebidae;
                                                                                                                                    Name=IL-6;
                                                                                                                                                                                                                                   26
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nilarity 55.4%;
Conservative 3
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23401
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By similarity.
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By similarity.
For a p (in Ref. 2)
Brown (in Ref. 2)
AKLOSQEEWLRHTII -
Ref. 2)
FS -> LR (in Ref. 2)
FS -> LR (in Ref. 2)
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pred. No. 2.2e
33; Mismatches
                                                                                                                                                                  Created)
Last sequence update)
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          sequencing .";
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No. 2.2
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                                              J.A.,
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                                                                                                               Euteleostomi;
Aotinae; Aotu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7;
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                             genes
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Immunogenetics

54:645-653 (2002).

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Best Local Sin
Matches 107;
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GO; GO:0005576; C:extracellular; IEA.
GO; GO:0005125; F:cytokine activity; IEA.
GO; GO:0005128; F:interleukin-6 receptor bi
GO; GO:0005955; P:immune response; IEA.
InterPro; IPR009079; 4 helix cytokine.
InterPro; IPR003573; II.6 MGF GCSF.
InterPro; IPR003574; Interleukin_6.
Pfam; PF00489; II.6; 1.
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PRINTS; PR00433; IL6GCSFMGF.

PRINTS; PR00434; INTERLEUKIN6.

ProDom; PD004356; Interleukin_6; 1.

SMART; SM00126; IL6; 1.

PROSITE; PS00524; INTERLEUKIN_6; 1.

NON_TER 1 1
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Q28403;
Q1-NOV-1996
Q1-NOV-1996
Q1-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

MEDLINE=96163018; PubMed=8575817;

King D.P., Schrenzel M.D., McKnight M.L., Reidarson T.H.,

Stott J.L., Ferrick D.A.;

"Molecular cloning and sequencing of interleukin 6 cDNA fr

"Molecular cloning and sequencing of interleukin 6 cDNA fr

the harbor seal (Phoca vitulina), killer whale (Orcinus or

Southern sea otter (Enhydra lutris nereis).";
                            ProDom; PD004356; Interleukin_6; 1.
SMART; SM00126; IL6; 1.
PROSITE; PS00254; INTERLEUKIN_6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Enhydra lutris (Sea otter).
Eukaryota; Metazoa; Chordata;
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                                                                                                                                            PRINTS; PR00433; IL6GCSFMGF.
PRINTS; PR00434; INTERLEUKIN6
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InterPro; IPR003573; IL6_MGF_GCSF.
InterPro; IPR003574; Interleukin_6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=34882;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Interleukin 6 (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunogenetics 43:190-195(1996).
EMBL; L46804; AAB01428.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AVOMSTK 479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                        INTERLEUKIN_6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Carnivora;
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0; Mismatches
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Pred. No. 3.5
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9;
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ia; Mustelidae; Lutrinae;
                                                                                                                                                                                                                                                                                                                                                                                                                  binding;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hanni K.D.,
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Best Local S
Matches 104
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Best Local
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01-OCT-2002
01-OCT-2002
01-MAR-2004
                                                                                                                                                                                                                                                                                                                                                               PRINTS; PRO0433; TL6GCSFMGF.
PRINTS; PR00434; INTERLEUKIN6.
PRODOM; PD004356; Interleukin_6; 1.
SMART; SM00126; IL6; 1.
PROSITE; PS00254; INTERLEUKIN_6; 1.
SEQUENCE 214 AA; 23765 MW; 5084
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR009079; 4 helix_cytokine.
InterPro; IPR003573; ITE MGF GCSF.
InterPro; IPR003574; InterPeukin_6.
Pfam; PF00489; IL6; 1.
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Submitted (MAR-2002) to the EM
EMBL; AF493992; AAN27192-1; --
HSSP; P05231; 1ALU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO; GO:0005576; C:extracellular; IEA.
GO; GO:0005125; F:cytokine activity; IEA.
GO; GO:0005138; F:interleukin-6 receptor
GO; GO:0006955; P:immune response; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Blood;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sus scrofa (Pig).
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                                                                                                                 408 MCESSKEALAENNLNLPKWAEKDGCFQSGFNEETCLVKIITGLLEFEVYLEYLQNRFESS
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                                    BEQARAVQMSTKVLIQFLQKKAKNLDAITTPDPTTNASLLTKLQAQNQWLQ 518
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  KGNVEAVQISTKALIQTLRQKGKNPDKATTPNPTTNAGLLDKLQSQNEWMK
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57.3%;
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e EMBL/GenBank/DDBJ
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Last annotation updat
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Pred. No. 2.1e
37; Mismatches
                                                                                                                                                                                                                                                                          Score 501.5; DB 1
Pred. No. 2.5e-27;
28; Mismatches 36
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                                                                                                                                                                                                                                                                                                                                                                      50849FB04D0BDD7F CRC64;
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                                                                                        YLDYLQKEYESN
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05-JUL-2004
05-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAS73282;
AAS73282;
29-MAR-2004
29-MAR-2004
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SEQUENCE
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Submitted (FEB-2004) to the EMBL/GenBank/DDBJ
EMBL; AY540191; AAS73282.1; -.
InterPro; IPR009799; 4 helix cytokine.
InterPro; IPR003573; II6_MGF_GCSF.
InterPro; IPR003574; Interleukin_6.
Pfam; PF00489; II6; 1.
                         SEQUENCE FROM N.A.
O'Brien R., Berger S., Griffin F.;
O'Brien R., nterleukin-6 gene.";
"Cervine interleukin-6 gene.";
Submitted (FBB-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, AY540191; AAS73282.1; -.
                                                                                                                                                                                                                                                                                                                 Cervus elaphus (Red deer).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia; Eutheria; Cetartiodactyla; Cervinae; Cervus.
                                                                                                                                                                                                                                                                                                                                                                                                                    29-MAR-2004 (TrEMBLrel.
Interleukin-6 (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PRO0433; IL6GCSFMGF.
PRINTS; PR00434; INTERLEUKIN6.
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                                                                                                                                                                                                                                                                                        Cervinae; Cervus.
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                                                                                                                                                                                                                                            NCBI_TaxID=9860;
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SM00126; IL6; 1.
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191 AA;
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(TrEMBLrel. 27,
(TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TrEMBLrel. 27, Created)
(TrEMBLrel. 27, Last sequence update)
(TrEMBLrel. 27, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16.9%;
49.7%;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 482.5;
Pred. No. 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5936607DB4D3C1A0 CRC64;
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hes 49;
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                                                                                                                                                                                                                                                                                                                     Euteleostomi;
cora; Cervidae;
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RESULT 31
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Best Local Similarity
                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collar between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
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01-NOV-1997
01-NOV-1997
05-JUL-2004
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SEQUENCE
                                                                                                                                            EMBL; D86569; BAA13118.1; -. HSSP; P05231; 1IL6.
                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=97392354; PubMed=9250586; Takakura H., Mori Y., Tatsumi M.; "Molecular cloning of caprine IL-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=116
                          PRINTS; PRO0433; ILGGCSFMGF.
PRINTS; PR00434; INTERLEUKIN
PRODOM; PD004356; Interleukin
SMART; SM00126; IL6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                  cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9925;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Caprinae; Capra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Capra hircus (Goat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Interleukin-6
                                                                                               InterPro; IPR009079;
InterPro; IPR003573;
InterPro; IPR003574;
 Acute phase;
                PROSITE; PS00254;
                                                                                     Pfam; PF00489; IL6; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IL6 CAPHI
                                                                                                                                                                                                                                                                                               Arch. Allergy Immunol. 113:409-416(1997).

FUNCTION: IL-6 is a cytokine with a wide variety of biological functions: it plays an essential role in the final differentiat of B-cells into Ig-secreting cells, it induces myeloma and plasmacytoma growth, it induces nerve cells differentiation, ir hepatocytes it induces acute phase reactants.

SUBCELULIAR LOCATION: Secreted.

SIMILARITY: Belongs to the IL-6 superfamily.
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191 AA;
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(Rel. 35, Last sequence update)
(Rel. 44, Last annotation update)
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 Cytokine;
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                                        Interleukin_6;
                INTERLEUKIN_6; 1.
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                                                                                                4 helix_cytokine.
IL6_MGF_GCSF.
Interleukin_6.
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49.7%; Pred. No. 4.6
Glycoprotein; Growth
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Best Local
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BOVIN
                                                                                                                                                                                                                    MEDINE-3076003; PubMed=1446077;
MEDINE-3076003; PubMed=1446077;
Proogmans L., Cludts I., Cleuter Y., Kettmann R., Burny A.;
Mucleotide sequence of bovine interleukin-6 cDNA.";

NA Seq. 2:411-413(1992).

INA Seq. 2:411-413(1992).

INA Seq. 2:411-416 is a cytokine with a wide variety of biological functions: it plays an essential role in the final differentiation of B-cells into Ig-secreting cells, it induces myeloma and plasmacytoma growth, it induces nerve cells differentiation, in hepatocytes it induces acute phase reactants.

In SUBCELLULAR LOCATION: Secreted.

In SUBCELLULAR LOCATION: Secreted.
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIGNAL
CHAIN
                                                                                                                This SWISS-PROT entry is copyright. It is produced through a c between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                            EMBL; X57317; CAA40572.1; PIR; A56610; A56610.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Holstein;
                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Bovinae;
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    P05231; IIL6.
P05231; IIL6.
Pro; IPR009079; 4 helix cytokine.
rPro; IPR003573; II6_MGF_GCSF.
rPro; IPR003574; Interleukin_6.
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Interleukin-6.
By similarity.
By similarity.
N-linked (GlcNAc.
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Matches 94
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01-APR-1993
01-JUN-1994
05-JUL-2004
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                                                                          This SWISS-PROT entry 18 copyright. 10 between the Swiss Institute of Bioinfo the European Bioinformatics Institute.
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SMART; SM00126; IL6;
PROSITE; PS00254; IN
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                                                                                                                                                                                                                                                                                                                       Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=94041419; PubMed=8225400;
Andrews A.E., Barcham G.J., Ashma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia; Eutheria;
Caprinae; Ovis.
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                                                                                                                                                                                                                                                                                                                                           Ebrahimi
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                        . Tounum
                                                                                                                                                                FUNCTION: IL-6 is a cytokine with a wide variety of biological functions: it plays an essential role in the final differentiation of B-cells into Ig-secreting cells, it induces myeloma and plasmacytoma growth, it induces nerve cells differentiation, in hepatocytes it induces acute phase reactants (By similarity). SUBCELLULAR LOCATION: Secreted.
                                                                                                       SWISS-PROT entry is copyright. It is produced sen the Swiss Institute of Bioinformatics and
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non-profit institutions as long as its content is in and this statement is not removed. Usage by and for comrequires a license agreement (See http://www.i-c
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By similarity.
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EMBL; X68723; CAA64662.1; -.
EMBL; A19159; CAA01443.1; -.
PIR; S29549; S29549
HSSP; P05231; 1116.
InterPro; IPR009079; 4 helix_cytokine.
InterPro; IPR003573; II6 MGF GCSF.
InterPro; IPR003574; Interleukin_6.
Pfam; PF00489; I16; 1.
Pfam; PF00489; I16; 1.
Premraj A., Sreekumar B., Rasool T.J.;
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ dat
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ dat
EMBL; AY347710; AAQ54301.1; -
InterPro; IPR009079; 4 helix cytokine.
InterPro; IPR003573; IT6_MGF_GCSF.
InterPro; IPR003574; Interleukin_6.
PRINTS; PR00489; IL6; 1.
PRINTS; PR00434; INTERLEUKIN6.
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PRINTS; PR00434; INTERLEUKIN6.
PRODOM; PD004356; Interleukin
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05-JUL-2004
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                                                                                                                  Bubalis bubalis (Domestic water buffalo).
Bubaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bubalus.
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(TrEMBLrel. 27, Last sequence update)
(TrEMBLrel. 27, Last annotation updat
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I - V (in Ref. 2).
M -> L (in Ref. 2).
M -> R (in Ref. 2).
S - R (in Ref. 2).
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Pred. No. 6.4e
35; Mismatches
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SMART; SM00126; IL6; 1.
PROSITE; PS00254; INTERLEUKIN_6;
SEQUENCE 208 AA; 23772 MW; 0
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AAQ54301;
02-MAR-2004
02-MAR-2004
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea

Bovidae; Bovinae; Bubalus.

NCBI_TaxID=89462;
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"Identification and molecular characterization of major
Indian water buffalo (Bubalus bubalis).";
of Indian water buffalo (Bubalus bubalis) databases.
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY347710; AAQ54301.1; -
EMBL; AY347710; AAQ54301.1; -
SEQUENCE 208 AA; 23772 MW; 0C3F0374C52E7342 CRC64;
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Best Local S
Matches 88
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InterPro; IPR003573; II.6 MGF GCSF.
InterPro; IPR003574; Interleukin_6.
Pfam; PP00489; II.6; 1.
PRINTS; PR00433; II.6GCSFMGF.
PRINTS; PR00434; INTERLEUKIN6.
PRODom; PD00434; INTERLEUKIN6.
PRODOm; PD004356; Interleukin_6; 1.
SMART; SM00126; II.6; 1.
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DISULFID
SEQUENCE
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15-JUL-1999
05-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; Y14139; CAA74571.1; -. HSSP; P05231; IALU.
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MEDLINE=98139533; PubMed=9472070;
Lohrengel B., Lu M., Roggendorf M.;
"Molecular cloning of the woodchuck cytokines: TNF-alpha, IFN-gamma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Marmota monax (Woodchuck).
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-i FUNCTION: IL-6 is a cytokine with a wide variety of biological functions: it plays an essential role in the final differentiat of B-cells into Ig-secreting cells, it induces myeloma and plasmacytoma growth, it induces nerve cells differentiation, it hepatocytes it induces acute phase reactants (By similarity).

-i- SUBCELLULAR LOCATION: Secreted.

-i- SIMILARITY: Belongs to the IL-6 superfamily.
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193
                                                  529
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 phase; Cytokine; Glycoprotein; Growth factor; Signal.
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                                                                                                        DRAEHVOSSSKALIEILKOEVKDPNKIVFPSPTANINLLAKLESONDWOKVMTMOLILSN
                                                                                                                                                        ARA---VQMSTKVLIQFLQKKAKNLDAITTPDPTTNASLLTKLQAQNQWLQDMTTHLILRS
                                                                                                                                                                                                                                                                                                                           ATAFPASELQREDGENSVTRNKPTR---ASSGKTRRQISYLIKEVFEMRKELCKNDETCI
FEDFLOFTLRAVRK 206
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(Rel. 38, Last sequence update)
(Rel. 44, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                 15.3%; Score 437.5; Larity 45.4%; Pred. No. 7.76 Conservative 39; Mismatches
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By similarity.
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Interleukin-6.
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01-OCT-2000
05-JUL-2004
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SMART; SM00126; IL6; 1.
PROSITE; PS00254; INTERLEUKIN 6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                         Hepatology 34:1049-1059(2001).
EMBL; AF012908; AAF24861.1; -.
EMBL; AF122896; AAF28873.1; -.
EMBL; AF333966; AAK52717.1; -.
HSSP; P05231; 1ALU.
                                                                                                                                                                                                                                                                                     Pfam; PF00489; IL6; 1.
PRINTS; PR00433; IL6GCSFMGF.
PRINTS; PR00434; INTERLEUKIN6.
                                                                                                                                                                                                                                                                                                                     GO; GO:0005576; C:extracellular; IEA.
GO; GO:0005125; F:cytokine activity; IEA.
GO; GO:0005128; F:interleukin-6 receptor binding; IEA.
GO; GO:0006955; P:immune response; IEA.
InterPro; IPR009079; 4 helix cytokine.
InterPro; IPR003573; IL6_MGF_GCSF.
InterPro; IPR003574; Interleukin_6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Augmented hepatic interferon gamma expression and T-cell influx characterize acute hepatitis progressing to recovery and residualifelong virus persistence in experimental adult woodchuck hepatifielong virus persistence in experimental adult woodchuck hepati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
Li D.H., Cullen J.M.;
Submitted (JAN-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Peripheral blood;
Li D.H., Cullen J.M.;
Submitted (JUL-1997) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9ЛННЗ;
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                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=21536769; PubMed=11679978;
Hodgson P.D., Michalak T.I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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Mammalia; Eutheria;
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                                                                   ARA--VOMSTKVLIQFLQKKAKNLDAITTPDPTTNASLLTKLQAQNQWLQDMTTHLILRS
                                                                                                                                            ATAFPASELQREDGENSVTRNKPTR---ASSGKTAGQISYLIKEVFEMRKELCKNDETCI
FEDFLQFTLRAVRK
                      FKEFLOSSLRALRO 542
                                             DRAEHVOFSSKALIEILKQEVKDPNKIVFPSPTANINLLAKLESONDWOKVMTMQLILSN
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Rodentia;
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Last annotation update)
                                                                                                                                                                                        Score 435.5; |
Pred. No. 1.1e
38; Mismatches
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Sciurognathi;
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thi; Sciuridae; Sciurinae;
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Matches 100
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
15-JUL-2004 (TrEMBLrel. 27, Last annotation update)
16-JUL-2004 (TrEMBLrel. 27, Last sequence update)
16-JUL-2004 (TrEMBLrel. 27, Last sequence update)
17-JUL-2004 (TrEMBLrel. 27, Last sequence update)
18-JUL-2004 (TrEMBLrel. 27, Last sequence update)
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Tetraodon nigroviridis (Green puffer).
Tetraodon nigroviridis (Green puffer).
Tetraodon (Control of the Control of th
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     ARR2568;

ARR2568;

ARR2568;

ARR2604 (TEMBLrel. 27, Last sequence update)

02-MAR-2004 (TEMBLrel. 27, Last amoutation update)

02-MAR-2004 (TEMBLrel. 27, Last annotation update)

02-MAR-2004 (TrEMBLrel. 27, Last annotation update)

02-MAR-2004 (TrEMBLrel. 27, Last annotation update)

02-MAR-2004 (TrEMBLrel. 27, Last annotation update)

Class I helical cytokine receptor number 21.

CRPA21.

CRPA21.

Tetraodon nigroviridis (Green puffer).

Tetraodon nigroviridis (Green puffer).

Eukaryota; Metazoa; Chordata; Cranitata; Euteleosteni;

Eukaryota; Neopterygii; Teleosteni; Euteleosteni;

Eukaryota; Neopterygii; Teleosteni; Euteleosteni;

Actinopterygii; Neopterygii; Percomorpha; Tetraodontiformes;

Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontidae; Te
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pred. No. 131;
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Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY374493; AAR25684.1; -.
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This SWISS-PROT entry is copyright. It is produced through a collaboration—the Swiss Institute of Bioinformatics and the EMBL outstation—the Buropean Bioinformatics Institute. There are no restrictions on its buropean Bioinformatics Institute. There are no restrictions on one way the European Bioinformatics Institute as its content is in no way use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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Search completed: December 9, 2004, 09:20:54
Job time : 252.038 secs
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REMBL; M26745; AAA41430.1; -.

REMBL; M26745; IRVERLEUKIN_6.

REMBL; M26745; INTERLEUKIN_6.

REMBL; M26745; INTERLEUKIN_6; 1.

REMBL; M26745; INTERLEUKIN_6; 1.

REMBL; M26745; INTERLEUKIN_6; 1.

REMBL; M26745; INTERLEUKIN_6; 1.

REMBL; M26745; AAA41430.1; -.

REMBL; M26745; AAA44130.1; -.

REMBL; M26745; AAA44430.1; -.

REMBL; M26745; AAA44430.1; -.

REMBL; M26745; AAA44430.1; -.

REMBL; M26745; AAA4444

REMBL; M26745; AAA444

REMBLEMEL M2675; AAA444

REMBL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             351 ATSLPVEFMPVPPGEDSKDVAAPHRQPLTSSERIDKQIRVILDGISALRKETCNKSNMCE 410
                                                                                                                                                                                                                                                                                                                                530 KEFLQSSLRALRQ 542 : | | | : :: | : | |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         470 QARAVQMSTKVLIQFLQKKAKNLDAITTPDPTTNASLLTKLQAQNQWLQDMTTHLILRSF 529
                                                                                                                                                                                                                                                               198 EEFLKVTMRSTRQ 210
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GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: December 9, 2004, 08:55:07; Search time 1.14568 Seconds (without alignments) 1091.766 Million cell updates/sec

Title: US-09-462-416-1
Perfect score: 67
Sequence: 1 EFGAGLVLGGOFM 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 00000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	BB	ID	Description
_	40	68.7	382	N	AC3118	nscription re
N	40	68.7	402	N	16	
ω	46	68.7	1171	_	QQKBFP	ate (fla
4	42		396	N	B75290	Ξ.
v	41	•	291	N	E71491	geranyl
o	41		313	N	S66962	membrane
7	41	61.2	347	N	D83605	
8	41		623	N	S56206	membrane
9	41		920	N	C70668	
10	40	59.7	232	Н	S28609	denyly]
11	40	59.7	492	Ŋ	A87471	hypothetical prote
12	40	59.7	579	N	B82085	0
13	40	59.7	1617	N	B86483	
14	39	58.2	220	N	E71857	e outer me
15	39	•	230	N	C64658	outer membrane pro
16	39	•	274	N	H72521	probable thiazole
17	39		308	N	H81685	conserved hypothet
18	39	•	622	N	B71326	probable V-type AT
19	39		770	N	S56805	
20	38.5	•	880	N	F83386	ical
21	38	•	127	N	A53952	٠.
22	38		147	N	AG3578	hypothetical prote
23	38		171	N	T11285	a
24	38		249	N	T09139	26S proteasome alp
25	38	56.7	249	N	G84667	proteasome su
26	38	56.7	272	N	A84747	hypothetical prote
27	38	56.7	298	N	AD2715	ter,
28	38	•	,	s	1	bable Fe(II) t
29			246		T06385	1

ALIGNMENTS

RESULT 2 D98169 frcR protein (AP196574) [imported] - Agrobacterium tumefaciens (strain C58, Cereon) C;Species: Agrobacterium tumefaciens C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004 C;Accession: D98169 R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001 A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tume A;Accession: D98169 A;Status: preliminary A;Accession: D99169 A;Residues: 1-402 KUR> A;Cross-references: UNIPROT:Q8U787; GB:AB007870; PIDN:AAK88878.1; PID:g15158645; GSPDB:Gt C;Genetics: A;Gene: AGR I_609 A;Map position: linear chromosome	Query Match 68.7%; Score 46; DB 2; Length 382; Best Local Similarity 80.0%; Pred. No. 3.6; Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0; Qy 2 FGAGLVLGGQ 11	RESULT 1 AC3118 AC3118 transcription regulator, ROK family Atu4567 [imported] - Agrobacterium tumefaciens (strai transcription regulator, ROK family Atu4567 [imported] - Agrobacterium tumefaciens (strai C;Species: Agrobacterium tumefaciens C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004 C;Accession: AC3118 C;Accession: AC3118 R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L. erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClellé; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001 A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, E

```
C;Species: Klebsiella pneumoniae
C;C;Date: 25-Feb-1985 #sequence revision 12-Apr-1996 #text change 09-Jul-2004
C;Caccession: S01997; S01836; S35903; S21414; A04461; S36947
C;Accession: S01997; Buchanan-Wollaston, V.; Ally, D.; Ally, A.; Beynon, R;Cannon, M.; Cannon, F.; Buchanan-Wollaston, V.; Ally, D.; Ally, A.; Beynon, Rucleic Acids Res. 16, 11379, 1988
Nucleic Acids Res. 16, 11379, 1988
A;Title: The nucleotide sequence of the nifJ gene of Klebsiella pneumoniae.
A;Reference number: S01997; MUID:89083580; PMID:3060860
A;Reference number: S01997; MUID:89083580; PMID:3060860
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C;Species: Klebsiella pneumoniae
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A; Residues: 1-405, 'A', 407-1171 <ARN>
A; Cross references: EMBL:X13303; NID:943820; PIDN:CAA31665.1; PID:943821
A; Cross references: EMBL:X13303; NID:943820; PIDN:CAA31665.1; PID:943821
A; Cross references: EMBL:X1303; NID:943820; PIDN:CAA31665.1; PID:943821
A; Cross references: Cannon, W.; Cannon, W.; Buck, M.
Mol. Microbiol. 7, 1007-1021, 1933
A; Reference number: S35903; MUID:93247479; PMID:8483412
A; Reference number: S35903; MUID:93247479; PMID:8483412
A; Reference number: S35903; MUID:93247479; PMID:8483412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Residues: 1-131 cCHA>
A; Residues: 1-131 cCHA>
A; Cross-references: EMBL:X13109
A; Cross-references: EMBL:X13109
A; Otos: the authors translated the codon ATT for res
A; Note: the authors translated the codon ATT for res
B; Wu, Y.; Yu, G.; Zhu, J.; Shen, S.C.
R; Wu, Y.; Yu, G.; Zhu, J.; Shen, S.C.
R; Wu, Y.; Yu, G.; Zhu, J.; Shen, S.C.
R; Wu, Y.; Yu, G.; Zhu, J.; Shen, S.C.
R; Wu, Y.; Yu, G.; Zhu, J.; Shen, S.C.
R; Wu, Y.; Yu, G.; Zhu, J.; Shen, S.C.
R; Wu, Y.; Yu, G.; Zhu, J.; Shen, S.C.
R; Reference number: S21414
A; Accession: S21414
A; Accession: S21414
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A; Residues: 1-117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: S01836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Shen, S.; Xue, Z.; Kong, Q.; Wu, Q.
Nucleic Acids Res. 11, 4241-4250, 1983
Nucleic Acids Res. 11, 4241-4250, 1983
A;Title: An open reading frame upstream from the nifH gene of Klebsiella pneumoniae.
A;Reference number: A04461; MUID:83246546; PMID:6306580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Molecule type: DNA
A,Residues: 1-127,129-135,'S',137-153,'TI',160,'IST',161-169 <WUY>
A,Residues: RMBL:XL6345; NID:g43864; PIDN:CAA34396.1; PID:g43865
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Best Local
                                                                                                                   A;Description: transfers one electron from pyruvate to flavodoxin
A;Bethway: nitrogen fixation
C;Superfamily: pyruvate (flavodoxin) dehydrogenase; ferredoxin 2[4Fe-4S] homology
C;Superfamily: pyruvate (flavodoxin) dehydrogenase; ferredoxin 2[4Fe-4S] homology
C;Keywords: 4Fe-4S; electron transfer; iron-sulfur protein; metalloprotein; oxidoreducta
C;Keywords: 4Fe-4S; homology <FER>
C;Keywords: ferredoxin 2[4Fe-4S] homology <FER>
C;Superfamily: ferredoxin 2[4Fe-4S] homology <FER>
C;Keywords: 4Fe-4S; homology <FER>
F;691.694,697,755/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted
F;691.694,697,755/Binding site: 4Fe-4S cluster (Cys) (covalent)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: A04461
                                                                                                                                                                                                                                                                                                                                                                              A;Gene: nifJ
C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:X01007;
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-127 <SHE>
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                                      Similarity
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80.0%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NID:g43860; PIDN:CAA25502.1; PID:g43861
   ; Score 46; DB; Pred. No. 11; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                       Indels
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hypothetical protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Aate: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Aate: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Aacession: B75290
C;Abccession: B75290
C;Abccession: B75290
R;White, O.; Bisen, J. J., Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dc
C;Abccession: B75290
R;White, O.; Bisen, J. J.; Lam, P.; McDonald, L.; Utterback, T.; Zale
C, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zale
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S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
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A;Map position: 1
C;Superfamily: te
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A; Residues: 1-396 < WHI>
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A;Reference number: A71570; MUID:99000809; PMID:9784136
A;Accession: E71491
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A;Title: Genome sequence of an obligate intracellular
                                                                                                                                                                                                                                                                                                                                                                                             A;Cross references: UNIPROT:084633; GB:AE001333; GB:AE001273; NID:93329068; PIDN:AAC6823; A;Experimental source: serotype D, strain UW-3/Cx
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A; Molecule type: DNA
A; Residues: 1-291 <ARN>
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C;Superfamily: geranyltranstransferase
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Best Local S
probable membrane protein YOR079c - yeast (Saccharo N;Alternate names: hypothetical protein O2960 C;Species: Saccharomyces cerevisiae C;Sate: 12-Jul-1996 #sequence_revision 12-Jul-1996 C;Accession: 866962
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T.; Zalewski,
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C.; Ma
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RESULT 8
S56206
                                                                C;Species: Saccharomyces cerevisiae
C;Date: 02-Sep-1995 #sequence_revision 19-Oct-1995
C;Accession: S56206
R,Murakami, Y; Naltou, M.; Hagiwara, H.; Shibata,
submitted to the EMBL Data Library, May 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable binding
C;Species: Pseudo
                  A; Reference number: A; Accession: S56206
                                                   submitted to the EMBL Data Library, May 1: A;Description: Analysis of the nucleotide
                                                                                                                                          probable membrane protein YFL049w - yeast (Saccharomyces cerevisiae)
C;Species: Saccharomyces cerevisiae
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A; Reference number: A82950;
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A;Map position: 15R
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A; Residues: 1-313 <BOH>
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A; Accession: S66962
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                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Experimental source:
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Experimental source: strain S288C
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50; MUID:20437337; PMID:10984043
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Pred. No. 23;
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C;Genetics:
A;Gene: par
C;Superfamil
C;Keywords:
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A,Accession: C70668
A,Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
A;Residues: 1-920 <COL>
A;Residues: 1-920 <COL>
A;Cross-references: UNIPROT:P96289; GB:Z83858; GB:AL123456; NID:g3261675; PIDN:CA
A;Experimental source: strain H37Rv
C;Genetics:
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C;Keywords: transmembrane protein
F;121-137/Domain: transmembrane #
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R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, Nature 393, 537-544, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probable mmpL7 protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
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A;Residues: 1-623 <MUR>
A;Cross-references: UNIPROT:P43554; EMBL:D50617; NID:g836685; PID:d1009830; PID:g836706;
                                                                                                                                                                                                                                                                                                                                                                                                                   phosphoadenylyl-sulfate reductase (thioredoxin) (EC 1.8.4.8) - Synec N;Alternate names: 3'-phosphoadenylylsulfate reductase, thioredoxin N;Contains: 3'-phosphoadenosine 5'-phosphosulfate sulfotransferase
                                                                                                                                                                          A; Cross-references: UNIPROT: Q55309; EMBL: M84476; NID: g154543;
                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-232 <NIE>
                                                                                                                                                                                                                                           A; Reference number: S28609; MUID:93099269; A; Accession: S28609
                                                                                                                                                                                                                                                                  R;Niehaus, A.; Gisselmann, G.; Schwenn, J.D.
Plant Mol. Biol. 20, 1179-1183, 1992
A;Title: Primary structure of the Synechococcus PCC 7942
A;Reference number: S28609; MUID:93099269; PMID:1463852
                                                                                                                                                                                                                                                                                                                                                                       C;Species: Synechococcus sp.
C;Date: 10-Sep_1999 #sequence_revision 10-Sep-1999
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                                                                                     Superfamily: 3'-phosphoadenosine 5'-phosphosulfate reductase; Superfamily: 3'-phosphoadenosine 5'-phosphosulfate reductase; sulfotransf
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Score 40; DB Pred. No. 23; 1; Mismatches
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2; Mismatches
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R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J. B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein CC1789 [imported] - Caulobacter crescentus C;Species: Caulobacter crescentus C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004 C;Accession: A87471
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A87471
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protein F5J5.15 (imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 C;Accession: B86483 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-492 < STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sensory box/GGDEF family protein VC2370 [imported] - Vibrio cholerae (strain N16961 sero
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A; Residues: 1-579 <HEI>
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A;Accession: B82085
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                                                                                                                                           B86483
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Pred. No. 48;
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0; Mismatches
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Pred. No.
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             Federspiel, N.A.; Kaul,
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          outer membrane protein - Helicobacter pylori (strain 26695)
C.Species: Helicobacter pylori
C.Species: Helicobacter pylori
C.Species: Helicobacter pylori
C.Species: Helicobacter pylori
C.Species: O9-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C.Accession: C64658
R.;Gomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.; Cromb, J.F.; White, O.; Kerlavage, A.R.; Dodson, R.A.; Sutton, M.G.; Glodek, A.A.; McK
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.J.; Fujii, C.; Bowman, C.; Watthey
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey
Nacure 388, 539-547, 1997
Nature 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser
A;Althe: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A;Accession: C64658
A;Accession: C64658
A;Accession: C64658
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.: C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Reference and analysis of chromosome 1 of the plant Arabidopsis.
A;Recession: B86481; MUID:21016719; PMID:11130712
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A;Cross-references: UNIPROT:Q9SKV5; GB:AE005172; NID:g6598587; PIDN:AAF18642.1; GSPDB:GNC
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                        probable outer membrane protein - Helicobacter pylori (strain J99)
(;Species: Helicobacter pylori
A;Variety: strain J99
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C;Accession: E71857
R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.;
R;Ahm, R.A.; Ling, L.S.L.; Moir, D.T.; Mills, S.D.; Jiang, Q.; Taylor, D.E.;
; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.;
Nature 397, 176-180, 1999
                                                                                                                                                                                                                                                                                                                                                             A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric pathon, Reference number: A71800; MUID:99120557; PMID:9923682
                                                                                                                                                                                                                A;Cross-references: UNIPROT:Q9ZKA5; GB:AE001531; GB:AE001439; NID:g4155617; PIDN:AAD0661:
A;Experimental source: strain J99
C;Genetics:
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Pred. No. 1.5e
3; Mismatches
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Smith, H.O.; Fraser,

C:>

A.; McKenney Watthey, L.

R.D.,

A; Molecule type: DNA A; Residues: 1-230 < TOM>

Gwin:

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RESULT 17
H81685
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A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Ae A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Accession: H72521
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A; Restdues: 1-308 <TET
A; Cross-references: UNIPROT: Q9PK72; GB: AE002328;
A; Experimental source: strain Nigg (MoPn)
                                                                                                                                                                                                                                                                                                       R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A;Reference number: A81500; MUID:20150255; PMID:10684935
A;Accession: H81685
                                                                                                                                                                                                                                                                                                                                                                                                                          conserved hypothetical protein TC0598 [imported] - Chlamydia muridarum (strain Nigg) C;Species: Chlamydia muridarum, Chlamydia trachomatis MoPh C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004 C;Accession: H81685
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A; Residues: 1-274 < KAW>
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Pred. No. 40;
0; Mismatches
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hypothetical protein PA2070 [imported] - Pseudomonas aeruginosa (strain PAO1)
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A;Gene: SGD:HCA4
A;Cross-references: SGD:S0003570; MIPS:YJL033w
A;Map position: 10L
C;Keywords: ATP; nucleotide binding; P-loop
F;85-92/Region: nucleotide-binding motif A (P-l
F;190-195/Region: nucleotide-binding motif B
F;194-197/Region: DEAD motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; MoLecule type: DNA
A; Molecule type: TOV>
A; Residues: 1-770 < TOV>
A; Residues: 1-770 < TOV>
A; Cross-references: UNIPROT: P20448; EMBL: Z49308; NID: g1008154; PIDN: CAA89324.1; PID: g1008
A; Chang, T.H.; Arenas, J.; Abelson, J.
R; Chang, T.H.; Arenas, J.; Abelson, J.
Proc. Natl. Acad. Sci. U.S.A. 87, 1571-1575, 1990
A; Title: Identification of five putative yeast RNA helicase genes.
A; Reference number: A34848; MUID: 90160368; PMID: 2406722
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A;Experimental source: strain Nichols
C;Genetics:
A;Gene: TP0429
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B71326
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C;Genetics:
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A;Residues: 192-380,'I',382 <CHA>
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A; Accession: S56805
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R;Pohl, T.M.; Aljinovic, G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probable RNA helicase CA4 - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein J1250; protein YJL033w
C;Species: Saccharomyces cerevisiae
C;Date: 08-Jul-1995 #sequence_revision 08-Sep-1995 #text_change
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A; Residues: 1-622 < COL>
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Best Local Similarity
Matches 7; Conserv
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Best Local
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Local Similarity 70.0%;
es 7; Conservative
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142
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53.8%;
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Pred. No. 1.1e+02
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A;Reference number: A82950; MUID:2043:
A;Reference number: A82950; MUID:2043:
A;Accession: F83386
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-880 <STO>
A;Cross_references: UNIPROT:091245; GE
A;Cross_references: UNIPROT:091245; GE
A;Experimental source: strain PAO1
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R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, adman, S.; Clson, M.V.

; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunisi A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunisi A;Reference number: A82950; MUID:20437337; PMID:10984043
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J. Cell Biol. 125, 1289-1301, 1994
A;Title: The Schizosaccharomyces pombe cdc3(+) gene encodes a profilin essential A;Reference number: A53952; MUID:94266961; PMID:8207058
A;Accession: A53952
A;Atctus: preliminary
A;Status: preliminary
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R;Skelton, J.; Churcher, C.M.; Barrell, B.G.; Rajandream, submitted to the EMBL Data Library, August 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:Z98762; PIDN:CAB38578.1; GSPDB:GN00066; SPDB:SPAC4A8.15c A;Experimental source: strain 972h-; cosmid c4A8
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A; Residues: 1-127 <BAL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A, Map position: 1
A, Introns: 5/1; 116/1
C, Superfamily: profilin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary;
A;Molecule type: DNA
A;Residues: 1-127 <SKE>
A;Residues: 1-127 (SKE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Reference number: Z21751
A; Accession: T38785
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Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Superiamity: profifer C; Keywords: actin binding;
AG3578
hypothetical protein BMEII0552 [imported] - Brucella melitensis (strain 16M)
hypothetical protein BMEII0552 [imported] - Brucella melitensis
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;Alternate names: cdc3 protein
                                                                                                                                                                    RESULT
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Best Local
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                                                                                                                                                                                                                                                                                      FGTGIILAGO 67
                                                                                                                                                                                                                                                                                                                                                         FGAGLVLGGQ 11
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64.3%;
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Pred. No. 1.5e+02;
1; Mismatches 1;
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2; Mis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
28;
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K.; Lim,
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C;Accession: AG3578
R;DelVecchio, V.O.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, r.
R;DelVecchio, V.O.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, r.
R;Accession: AG3578
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitensi A;Reference number: AD3252; PMID:11756688
A;Accession: AG3578
A;Accession: AG3578
A;Accession: AG3578
A;Molecula type: DNA
A;Molecula type: DNA
A;Residues: 1-147 < KUR>
A;Cross-references: UNIPROT:Q44701; UNIPROT:Q8FVUO; GB:AE008918; PIDN:AAL53794.1; PID:g1:
A;Experimental source: strain 16M
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A; Map position: Il
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             submitted to the EMBL Data Library, July 1998
A;Description: The complete mitochondrial genome
A;Reference number: Z17258
A;Accession: T11285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: DNA
A;Residues: 1-98,'A',100-101,'CYA',105-171 <SOR>
A;Cross-references: EMBH:AF069428; PIDN:AAD09992.1; PID:g3219527;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Reference number:
A; Accession: T43695
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Best Local
                                                                                                  T09139
26S proteasome alpha chain - spinach
26S proteasome alpha chain - spinach
C;Species: Spinacia oleracea (spinach)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: T09139
C;Accession: T09139
C;Accession: T09139
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R;Ito, N.; Tomizawa, K.; Tanaka, K.; Matsui, M.; plant Mol. Biol. 34, 307-316, 1997
A;Title: Characterization of 26S proteasome alfa-
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Best Local S
Matches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Superfamily: NADH dehydrogenase (ubiquinone) chain 6; Reywords: membrane-associated complex; mitochondrion; NAD; oxidative
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6; Conserv
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8; Conserv
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66.7%;
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57.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 38; DB pred. No. 38; 3; Mismatches
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38;
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26S proteasome alfa-

and

EFGAGLVLGGQ 11

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A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487; PMID:10617197 A;Accession: G84667
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A; Residues: 1-272 <STO>
                                                                                                                                                                                                                                                                                                                                                         A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana A;Reference number: A84420; MUID:20083487; PMID:10617197 A;Accession: A84747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tal euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Ve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Accession: A84747
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A; Residues: 1-249 <STO>
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C;Superfamily: multicatalytic endopeptidase complex chain C9
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A; Residues: 1-249 < ITO>
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;Species: Arabidopsis thaliana (mouse-ear cress)
;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
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Matches
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Similarity 63. 7; Conservative
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Score 38; DB Pred. No. 59; 3; Mismatches
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A;Molecule type: mRNA, A;Molecule type: mRNA, A;Residues: 1-348 <COH>
A;Cresidues: 1-348 <COH>
A;Cross-references: UNIPROT:065348; EMBL:AF065444; NID:g3153888; PIDN:AAC17441.1; A;Experimental source: cultivar Sparkle C;Genetics: A;Gene: Ritl R;Gene: Ritl R;Gene: Ritl R;Gene: Ritl R;Gene: Ritl R;Gene: Ritl R;Gene: R;G
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A;Experimental source: strain C58 (Dupont)
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R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L. erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClella
hypothetical protein F28A12.4 - C;
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_rev
C;Accession: T28954
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A;Title: The role of iron-deficiency stress responses
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C;Accession: T06385
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C;Species: Pisum sativum (garden pea)
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C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
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A; Accession: T06385
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                          #sequence_revision
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56.7%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56.7%;
77.8%;
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Pred. No.
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Pred. No.
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74;
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-389 cSAM'>
A;Residues: 1-380 cSAM'>
A;Residues: 1-380 cSAM'>
A;Experimental source: strain Bristol N2; clone F28A12
A;Genetics:
A;Gen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R,Sammons, L.; Murray, J.
submitted to the EMBL Data Library, July 1996
A,Description: The sequence of C. elegans cosmid F28A12.
A,Reference number: Z20547
A,Accession: T28954
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T40924
nuclear localization protein - fission yeast (Schizosaccharomyces pombe)
c;Specises: Schizosaccharomyces pombe
c;Specises: Schizosaccharomyces pombe
C;Specises: Schizosaccharomyces pombe
C;Accession: T40924
C;Accession: T40924
A;Reference number: Z21957
A;Reference number: Z21957
A;Accession: T40924
A;Access
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A; Residues: 1-390 < VOL-
A; Experimental source: strain 972h-; cosmid c1281
A; Map position: 3
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Best Local S
Matches 7
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                                                                                                                                                                                                                                                                                                                                                        integral membrane protein (AJ272047) [imported] - Agrobacterium tumefaciens (strain C58, C; C) [integral membrane protein tumefaciens C; C) [integral membrane protein tumefaciens C; C] [integral membrane protein tumefaciens compared to the protein and sequence revision 30-Sep-2001 #text_change 09-Jul-2004 [integral membrane compared to the plant pathogen and Blanchard, M.; Qurollo, B.; Goldman, C; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; A.; Liu, P.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 32-2328, 2001 [integral membrane sequence of the plant pathogen and Blotechnology Agent Agrobacterium tumesticine compared for the plant pathogen and Blotechnology Agent Agrobacterium tumesticine compared for the plant pathogen and Blotechnology Agent Agrobacterium tumesticine compared for the plant pathogen and Blotechnology Agent Agrobacterium tumesticine compared for the plant pathogen and Blotechnology Agent Agrobacterium tumesticine compared for the plant pathogen and Blotechnology Agent Agrobacterium tumesticine compared for the plant pathogen and Blotechnology Agent Agrobacterium tumesticine compared for the plant pathogen and Blotechnology Agent Agrobacterium tumesticine compared for the plant pathogen and Blotechnology Agent Agrobacterium tumesticine compared for the plant pathogen and Blotechnology Agent Agrobacterium tumesticine compared for the plant pathogen and Blotechnology Agent Agrobacterium tumesticine compared for the plant pathogen and Blotechnology Agent Agrobacterium tumesticine compared for the plant pathogen and Blotechnology Agent Agrobacterium tumesticine compared for the plant pathogen and Blotechnology Agent Agrobacterium tumesticine compared for the plant pathogen and Blotechnology Agent Agrobacterium tumesticine compared for the plant pathogen and Blotechnology Agent Agrobacterium tumesticine compared for the plant pathogen and Blotechnology Agent Agrobacterium tumesticine compared for the plant pathogen and Blotechnology Agent
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A;Cross-references: UNIPROT:Q8UGB3; GB:AE007869; PIDN:AAK866928.1; C;Genetics: A;Gene: AGR C_2083 A;Gene: AGR C_2083 A;Map position: circular chromosome
                                                                                                                                                                                                                  A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-494 < KUR>
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Local Similarity 58.3%;
es 7; Conservative
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les 6; Conserv
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Pred. No. 83;
1; Mismatches
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Pred. No. 83;
4; Mismatches
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. 83;
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hypothetical protein flop12.2 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: G96498
C;Accession: G96498
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C;Accession: G96498
R;Theologis, A.; Ecker, J.R.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.,
Chin, C.W.; Chung, M.K.; Conm, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.,
A;Authors: Hunter, J.L.; Johkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
A;Authors: Hunter, J.L.; Johkins, J.; Johnson-Hopson, C.; Khan, S.; Maiti, R.; Marziall,
A;Authors: Munter, J.L.; Johkins, J.; Johnson-Hopson, J.S.; Maiti, R.; Marziall,
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziall,
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Sequence and analysis of Chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; pMID:11130712

A;Accession: G96498
A;Accession: G964
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A;Reference number: AD3252; PMID:11756888

A;Recession: AB3463

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A;Molecule type: DNA
A;Residues: 1-630 «KUR»
A;Residues: 1-630 «KUR»
A;Cross-references: UNIPROT:08YF36; GB:AE008917; PIDN:AAL52872.1; PID:917983715;
A;Experimental source: strain 16M
A;Experimental source: strain 16M
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A;Molecule type: DNA
A;Residues: 1-748 <STO>
A;Cross-references: UNIPROT:Q9XIG6; GB:AE005173; NID:g5080761; PIDN:AAD39271.1; GSPDB GN(
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A; Map position: 1
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; Pred. No. 1e+02;
1; Mismatches 1
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Pred. No. 1.3e+02;
1; Mismatches 0;
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RESULT 36
D64012
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A;Residues: 1-1195 <KAN>
A;Residues: 1-1195 <KAN>
A;Cross-references: UNIPROT:Q55786; EMBL:D64002; GB:AB001339; NID:g1001612; PIDN:BAA1043
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Superfamily: cobalamin-dependent methionine synthase; cobalamin-binding homology
C;Keywords: methyltransferase
F;737/Binding site: methylcobalamin cobalt (His) (axial ligand) #status predicted
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Nature 413, 848-852, 2001

A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.;
A;Title: Complete genome sequence of a multiple drug resistant
A;Title: Complete 3B0502, MUID:21534947, PMID:11677608
hypothetical protein H10704 - Haemophilus influenzae (strain Rd KW20) C;Species: Haemophilus influenzae A;Variety: strain Rd KW20 A;Variety: strain Rd KW20 C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004 C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004 C;Accession: D64012; T09409 C;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.;
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A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997
C;Accession: 876592
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A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocysti
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A; Residues: 1-754 < PAR>
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h, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.
S.; Moule, S.; O'Gaora, P.
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K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.;
A Res. 3, 109-136, 1996
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1; Mismatches 1
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  R.A.; Kirkness, E.F.; Kerlavage,
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Watanabe, A.; )
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A.; Yamada, M.; Yasuda
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A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkiok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; V. A;Title: Comparative genomics of Listeria species
                                                         A;Residues: 1-181 <GLA>
A;Cross-references: UNIPROT:Q928T7; GB:AL592022; PIDN:CAC97672.1; PID:g16414967; GSPDB:GN
A:Experimental source: strain Clip11262
                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AH1737
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                                                                                                                                                           A; Molecule type: DNA
                                                                                                                                                                                A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                        R;Glaser,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NADH-dependent FMN reductase homolog lin2445 [imported]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
                                                                                                                                                                                                                                                                                                                                                                                       R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, Dominguez-Bernal, G.; Duchaud, E.; Durand, L.;
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24

FGGGLGIGGGF

34

MUID:21537279;

F.; Kurapkat, G.; Madueno, rrez, A.; Vazquez-Boland, J

ō, Е.;

Maitournam, Voss, H.; W

m, A.; Mat Wehland,

Dussurget, O.; Entian,

Berche, P.; tian, K.D.;

Bloecker, Fsihi, H.;

Listeria innocua

(strain Clip1)

FGAGLVLGGQF 12

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RESULT 37
JS0297
                                                                                                                                                                                              A;Title: Characterization of an infection structure-specific A;Reference number: JS0297; MUID:90034196; PMID:2806914 A;Accession: JS0297
                                                                                                                                                                                                                                                                                         infection structure-specific protein - rust fungus (Uromyces appendiculatus)
C;Species: Uromyces appendiculatus
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
C;Accession: JS0297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; SA;Title: Whole-genome random sequencing and assembly of Haemophilus A;Reference number: A64000; MUID:95350630; PMID:7542800
A;Accession: D64012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-61 < TIGR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Note: HI0704
                                                                                                                                      A; Cross-references: UNIPROT: P14777
                                                                                                                                                          A; Residues: 1-150 < BHA>
                                                                                                                                                                          A; Molecule type: DNA
                                                                                                                                                                                                                                                                       R; Bhairi, S.M.; Staples, R.C.; Freve,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Cross-references: UNIPROT: P44040; GB: U32753;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
  Query Match
Best Local S
Matches 7
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Matches
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                                                                                                                                                                                                                                                         237-243, 1989
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  Similarity
7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAGLVLGGQFM 13
                                                                                                                      protein is involved
    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                      63.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55.2%;
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  Score 37; DB Pred. No. 49; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <u>..</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 37; DB Pred. No. 21; 0; Mismatches
                                                                                                                      in the
                                                                                                                                                                                                                                                                       P.; Yoder, O.
                                                                                                                      development
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GB:L42023; NID:g1573701; PIDN:AAC22367.1;
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••
                                      Length 150;
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    Indels
                                                                                                                      of infection
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                                                                                                                                                                                                                                     gene
  0;
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Gaps
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Page 10

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ALL14/1

C.Species: Listeria innocua
C.Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C.Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C.Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Date: C.Dat
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C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: A72786
C;Accession: A72786
R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah
R; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; X
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; X
awa, B.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; X
awa, Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
A; Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
A; Reference number: A72450; MUID:99310339; pMID:10382966
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A;Molecule type; DNA
A;Residues: 1-233 <KAW>
A;Residues: 1-233 <KAW>
A;Cross-references: UNIPROT:Q9YFH4; DDBJ:AP000058; NID:g5103388; PIDN:BAA79187.1; PID:g5
A;Experimental source: strain K1
A;Experimental source: strain K1
C;Gene: APE0270
A;Gene: APE0270
C;Superfamily: maltose transport protein malG
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Best Local Similarity 58.3%;
Matches 7; Conservative
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Matches 8
Search completed: December 9, 2004, 09:21:45
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es 7; Conservation
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8; Conservative
                                                                                                                                                  159 FGMGLVFGG 167
                                                                                                                                                                                                                          FGAGLVLGG 10
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pred. No. 59;
2; Mismatches 3; Indels
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pred. No. 75;
0; Mismatches
                                                                                                                                                                                                                                                                                                         Score 37; DB 2;
pred. No. 83;
0; Mismatches 2
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